

```

1 MPARRLLLLLLPGLGIFGSTVTLPETLLFVSTLDGSLHAVSKRTG 50
  |||||
1 MPARRLLLLLLPGLGIFGSTVTLPETLLFVSTLDGSLHAVSKRTG 50
  |||||

51 SIKWTLKEDPVLQVPTHVEEPAFLDPNDGSLYTLGSKNNEGLTKLPFTI 100
  |||||
51 SIKWTLKEDPVLQVPTHVEEPAFLDPNDGSLYTLGSKNNEGLTKLPFTI 100
  |||||

101 PELVQASPCRSSDGILYMGKKQDIWYVIDLLTGEKQQTLSAFADSLCPS 150
  |||||
101 PELVQASPCRSSDGILYMGKKQDIWYVIDLLTGEKQQTLSAFADSLCPS 150
  |||||

151 TSLLYLGRTEYTTIMYDTKTRELWNATYFDYAASLPEDEGDYKMSHFVS 200
  |||||
151 TSLLYLGRTEYTTIMYDTKTRELWNATYFDYAASLPEDEGDYKMSHFVS 200
  |||||

201 NGDGLVVTVDSEGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVEL 250
  |||||
201 NGDGLVVTVDSEGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVEL 250
  |||||

```

FIG. 1

103230 1511200

```

251 RYLTMSGEVGRITWKYPPFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 RYLTMSGEVGRITWKYPPFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300

301 HEGVAVVPRGSTLP LLEGPTDGV TIGDKGECVITPSTDVKFDPGLKSKN 350
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 HEGVAVVPRGSTLP LLEGPTDGV TIGDKGECVITPSTDVKFDPGLKSKN 350

351 KLNILRNWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKS F 400
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 KLNILRNWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKS F 400

401 EE..TLLQMTS 409
    || :|::||
401 EEVINLVDQTS 411

```

FIG. 1 (CONT.¹)

```

5  QLQSVSSAIHLCDKKKMWELSNIPVNHGPQEECSGSSQLHENSGBPETS 54
   :|||||
313 KLQSVSSAIHLCDKKKMWELSNIPVNHGPQEECSGSSQLHENSGBPETS 362
55  SLPAPQDNDFLSRKAQDCYFMKLHHCPCGNHSDWSTISGSQRAAFCDHKTT 104
   :|||||
363 SLPAPQDNDFLSRKAQDCYFMKLHHCPCGNHSDWSTISGSQRAAFCDHKTT 412
105 PCSSAIINPLSTAGNSERLQPGIAQQWIOSKREDIVNQWTEACLNQSLDA 154
   :|||||
413 PCSSAIINPLSTAGNSERLQPGIAQQWIOSKREDIVNQWTEACLNQSLDA 462
155 LLSRDLIMKEDYELVSTKPTRTSKVRQLDITTDIQEEFAKIVIQKLKDN 204
   :|||||
463 LLSRDLIMKEDYELVSTKPTRTSKVRQLDITTDIQEEFAKIVIQKLKDN 512
      205 KQMGLOYPEILVVSRSPSINLLQNKSM 232
         :|||||
      513 KOMGLOYPEILVVSRSPSINLLQNKSM 540

```

FIG. 2

105200 1984260

```

1  MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIRSMQKYLEDR 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIRSMQKYLEDR 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 GEVTFEKIFSQKLGYLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEE 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 GEVTFEKIFSQKLGYLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEE 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 RVARSR EIFDSYIMKELLACSHPF S K S A T E H V Q H L G K K Q V P D L F Q P Y I 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 RVARSR EIFDSYIMKELLACSHPF S K S A T E H V Q H L G K K Q V P D L F Q P Y I 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 EEICQNLRG D V F Q K F I E 167
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 EEICQNLRG D V F Q K F I E 167

```

FIG. 3

```

1 MGLVSSKKPDKEKPIEKDKGQWSPLKVSQDKDAPPLPPLVVFVFNHLLTPP 50
  |||
1 MGLVSSKKPDKEKPIEKDKGQWSPLKVSQDKDAPPLPPLVVFVFNHLLTPP 50
  |||
51 PPDEHLEDKHFVVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARS 100
  |||
51 PPDEHLEDKHFVVVALYDYTAMNDRDLQMLKGEKLQVLKGTGDWWLARS 100
  |||
101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150
  |||
101 VTGREGYVPSNFVARVESLEMERWFFRSQGRKEAERQLLAPINKAGSFLI 150
  |||
151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYIISPRITFPSLQA 200
  |||
151 RESETNKGAFSLSVKDVTTQGELIKHYKIRCLDEGGYIISPRITFPSLQA 200
  |||
201 LVQHYS..... 206
  |||||
201 LVQHYSKKGDLGCQRLTLPVCRPAPQNPWAQDEWELPRQSLRIVRKLGS 250
  |||
207 .....SYKNNMKVAIKTLKEGTSPEAFGEANVMKAIQHERLVR 249
  : |||
251 QFGEVMMGYKNNMKVAIKTLKEGTSPEAFGEANVMKAIQHERLVR 300

```

FIG. 4

250 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRISLPRLLIDMSAQIAEGMAY 299
 |||||
 301 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRISLPRLLIDMSAQIAEGMAY 350
 |||||
 300 IERMNSIHRDLRAANILVSEALCCKIADFGRLARIIDSEYTAQEGAKFPIK 349
 |||||
 351 IERMNSIHRDLRAANILVSEALCCKIADFGRLARIIDSEYTAQEGAKFPIK 400
 |||||
 350 WTAPEAIHFGVFTIKADVWSFGVLLMEVVTYGRVPYPGMSNPEVIRNLER 399
 |||||
 401 WTAPEAYHFGVFTIKADVWSFGVLLMEVVTYGRVPYPGMSNPEVIRNLER 450
 |||||
 400 GYRMPRPDTCPPELYRGVIAECWRSRPEERPTFEFLQSVLEDFYTATERQ 449
 |||||
 451 GYRMPRPDTCPPELYRGVIAECWRSRPEERPTFEFLQSVLEDFYTATERQ 500

450 YELQP 454

||||

501 YELQP 505

FIG. 4 (CONT.)

```

1  MENFQVEKIGEGTYGVVYKARKNLTEGEVVALKKIRLDTETEGVPSTAIR 50
  |||||
1  MENFQVEKIGEGTYGVVYKARKNLTEGEVVALKKIRLDTETEGVPSTAIR 50
  |||||

51  EISLLKELNHPNIVKLLDVIHTENK 75
  |||||
51  EISLLKELNHPNIVKLLDVIHTENK 75
  |||||

```

FIG. 5

```

1 MTRDEALPDHSAQDFYENYEPKEILGRGVSSVRRRCIHKPTSQEYAVKV 50
  |||||
1 MTRDEALPDHSAQDFYENYEPKEILGRGVSSVRRRCIHKPTSQEYAVKV 50
  |||||
51 IDVTGGGSFSPPEVRELREATLKEVDILRKVSGHPNISIQLKDTYETNTF 100
  |||||
51 IDVTGGGSFSPPEVRELREATLKEVDILRKVSGHPNI.IQLKDTYETNTF 99
  |||||
101 FFLVFDLMKRGELFD 115
  |||||
100 FFLVFDLMKRGELFD 114
  |||||

```

FIG. 6

FIG. 7

22 AVGCILAEALLAHRPLLPGTSEIHQIDLIVQLLGTSPSENWPFGSKLPLVG 71
 |||||
 197 AVGCILAEALLAHRPLLPGTSEIHQIDLIVQLLGTSPSENWPFGSKLPLVG 246
 |||||
 72 QYSLRKQPYNNLKHKFPWLSEAGIRLLHFLFMYDPKKRATAGDCLESSYF 121
 |||||
 247 QYSLRKQPYNNLKHKFPWLSEAGIRLLHFLFMYDPKKRATAGDCLESSYF 296
 |||||
 122 KEKPLRLPISGVCEGCREPG 141
 |||||
 297 KEKPLRLPISGVCEGCREPG 316

FIG. 8

```

1 VFLGRCSVKFEFEKINRIGEGTYGIYRARDTQTDEIVALKKVRMDKEK 50
  |||||
1 VFLGRCSVKFEFEKINRIGEGTYGIYRARDTQTDEIVALKKVRMDKEK 50
  |||||

51 GIPISLREITLLRLRHPNII 72
  |||||
51 GIPISLREITLLRLRHPNIV 72
  |||||

```

FIG. 9

```

1 MGEAEKFHYISCDLDINVLKIGSLEGRQKS YKAVLEDPMLKFSGLY 50
| | | | | | | | | | | | | | | | : | | | | | | | | | |
1 MGEAEKFHYISCDLDINVLKIGSLEGRQKS YNAVLEDPMLKFSGLY 50
. . . . .
51 QETCSDLVYCQVFAEGKPALPVRTSYKAFSTRWNWNEWLKL PVKYPDL 100
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 QETCSDLVYCQVFAEGKPALPVRTSYKAFSTRWNWNEWLKL PVKYPDL 100
. . . . .
101 PRNAQVALTIWDVYGPKAVPVGGTTVSFLGKYGMFRQGMHDLKVWP NVE 150
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
101 PRNAQVALTIWDVYGPKAVPVGGTTVSFLGKYGMSRQGMHDLKVWP NVE 150
. . . . .
151 ADGSEPTKTPGRTSSSTLSEDQMSRLAKLTKAHRQGHMV KVDWLDR LTFRE 200
| | | | | : | | | | | | | | | | | | | | | | | | | | | |
151 ADGSEPTKTPGRTSSSTLSEDQMSRLAKLTKAHRQGHMV KVDWLDR LTFRE 200
. . . . .
201 IEMINESVKRSSNFMYLMGGFCVKDDKEYGI VYEKGDESPIL TSF 250
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
201 IEMINESVKRSSNFMYLMGGFCVKDDKEYGI VYEKGDESPIL TSF 250
. . . . .
251 ELVKVPDQPOMSL ENLVESKH HNLPRSL RSGPSDH DLKPY P SPRDQL KNIV 300
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
251 ELVKVPDQPOMSL ENLVESKH HNLPRSL RSGPSDH DLKPY P SPRDQL KNIV 300

```

FIG. 10

301	SYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIWDLPOEAKQALA	350
301	SYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIWDLPOGAKQALA	350
351	LLGKNWPMDDVEDSLELISSHYTNPTVRRYAVARLQADDEDLLMYLLQLV	400
351	LLGKNWPMDDVEDSLELISSHYTNPTVRRYAVARLQADDEDLLMYLSQLV	400
401	QALKYENFDDIKNGLEPTKKDSQSSVSNVSGNSGINSAEIDSSQIITSPL	450
401	QALKYENFDDIKNGLEPTKKDSQSSVSGNVSGNSGINSAEIDSSQIITSPL	450
451	PSVSSPPPPASKTKEVPDGENLEQDLCTFLISPACKNSTLANLYLYWYVIVE	500
451	PSVSSPPPPASKTKEVPDGENLEQDLCTFLISPACKNSTLANLYLYWYVIVE	500
501	CEDQDQTQORDPKTHEMYLNVMMRRFSQALLKGDKSVRMRSLLAAQQT FVD	550
501	CEDQDQTQORDPKTHEMYLNVMMRRFSQALLKGDKSVRMRSLLAAQQT FVD	550

FIG. 10 (CONT.)¹

```

551 RLVHLMKAVQRESGNRKKNERLQALLGDNEKMNLSDVELLPLEPQVK 600
|||||
551 RLVHLMKAVQRESGNRKKNERLQALLGDNEKMNLSDVELLPLEPQVK 600
|||||
601 IRGII PETATL FKSALMPAQLFFKTEDGCKYPVIFKHGDDDLRQDQILQI 650
|||||
601 IRGII PETATL FKSALMPAQLFFKTEDGCKYPVIFKHGDDDLRQDQILQI 650
|||||
651 ISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSVPAEVLDTESI 700
|||||
651 ISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSVPAEVLDTESI 700
|||||
701 QNFFRKYAPSENGPNCISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLL 750
|||||
701 QNFFRKYAPSENGPNCISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLL 750
|||||
751 LTKTG 755
|||||
751 LTKTG 755

```

FIG. 10 (CONT. ²)

```

1  MGEAEKFHYISCDLDINVLKIGLEGKREQSYKAVLEDPMLKFSGLY 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MGEAEKFHYISCDLDINVLKIGLEGKREQSYNAVLEDPMLKFSGLY 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51  QETCSDLYVTCQVFAEGKPLALPVRTSYKAFSTRWNNEWMLKLPVKYPDL 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51  QETCSDLYVTCQVFAEGKPSALPVRTSYKAFSTRWNNEWMLKLPVKYPDL 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 PRNAQVALTIWDVYGP GKAVPVGGTTVSLFGKYGMRQGMHDLKVWP NVE 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 PRNAQVALTIWDVYGP GKAVPVGGTTVSLFGKYGMRQGMHDLKVWP NVE 150
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 ADGSEPTKTPGRTSSTLSE DQMSRLAKLTKAHRQGHMVKVDWLDRLTFRE 200
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 ADGSEPTKTPGRTSSTLSE DQMSRLAKLTKAHRQGHMVKVDWLDRLTFRE 200
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 IEMINESVKRSSNFM YLMGGFRCVKCDDKEYGIVYEEKDGESSPILTSF 250
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 IEMINESVKRSSNFM YLMGGFRCVKCDDKEYGIVYEEKDGESSPILTSF 250
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 ELVKVPDPQMSLENL VESKHHNLPRLSRGSPSDHDLKPYSPRDLKNIV 300
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 ELVKVPDPQMSLENL VESKHHNLPRLSRGSPSDHDLKPYSPRDLKNIV 300
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

FIG. 11

301 SYPPSKPPTYEEQDLVWEFRYILTQDKALTKILTSTVIWDLPOEAKQALA 350
 |||||
 301 SYPPSKPPTYEEQDLVWEFRYILTQDKALTKILTSTVIWDLPOGAKQALA 350
 |||||
 351 LLGKNPMDVEDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLLQLV 400
 |||||
 351 LLGKNPMDVEDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLSQLV 400
 |||||
 401 QALKYENFDDIKNGLEPTKKDSQSSVSENVNSGINSAEIDSSQIITSPL 450
 |||||
 401 QALKYENFDDIKNGLEPTKKDSQSSVSENVNSGINSAEIDSSQIITSPL 450
 |||||
 451 PSVSSPPPPASKTKEVPDGENLEQDLCTFLISPRACKNSTLANYLYWYVKII 500
 |||||
 451 PSVSSPPPPASKTKEVPDGENLEQDLCTFLISPRACKNSTLANYLYWYV.IV 499
 |||||

FIG. 11 (CONT.)¹

```

1  MGNAAAKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQFERIKTL 50
  |||
1  MGNAAAKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQFERIKTL 50
  |||
51 GTGSFGRVMLVKHKETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVN 100
  |||
51 GTGSFGRVMLVKHKETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVN 100
  |||
  101 FPFLVKLEFSFKDNSNLYMMEYVPPGGEMFSLRIGRF 139
    |||
  101 FPFLVKLEFSFKDNSNLYMMEYVPPGGEMFSLRIGRF 139
    |||

```

FIG. 12

```

1  MVFENGLKIKICEAVSLKPTAWSLRHAVGPRPQTFLLDPYIALNVDDSR 50
  |||||
1  MVFENGLKIKICEAVSLKPTAWSLRHAVGPRPQTFLLDPYIALNVDDSR 50
  |||||
51 IGQTATKQKTNSPAWHDEFVTDVCNGRKIELAVFHDAPIGYDDFVANCTI 100
  |||||
51 IGQTATKQKTNSPAWHDEFVTDVCNGRKIELAVFHDAPIGYDDFVANCTI 100
  |||||
101 QFEELLQNGSRHFEDWIDLEPEGRVYVVIIDLSGSSGEVKIPNSAFCEER 150
  |||||
101 QFEELLQNGSRHFEDWIDLEPEGRVYVVIIDLSGSSGEAPKDNEERVFRER 150
  |||||
151 VEMR 154
  :: |
151 MRPR 154

```

FIG. 13

1	MILIPRMLLVFLLLPILSSAKAQNPAICRYPLGMSGGQIPDEDITASS	50
1	MILIPRMLLVFLLLPILSSAKAQNPAICRYPLGMSGGQIPDEDITASS	50
51	QWSESTAACYGRLDSEEGDGAWCPEIPVEPDDLKEFLQIDLHLHLFITLV	100
51	QWSESTAACYGRLDSEEGDGAWCPEIPVEPDDLKEFLQIDLHLHLFITLV	100
101	GTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDI	150
101	GTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDI	150
151	FLKLEPPIVARFVRFIPTVDHSMNVCMRVELYGCVWLGLVSYNAPAGQ	200
151	FLKLEPPIVARFVRFIPTVDHSMNVCMRVELYGCVWLGLVSYNAPAGQ	200
201	QFVLPGGSIIYLNDSVYDGAVGYSMT EGLQLTDGVSGLDDFTQTHEYHV	250
201	QFVLPGGSIIYLNDSVYDGAVGYSMT EGLQLTDGVSGLDDFTQTHEYHV	250
251	WPGYDVYGVWRNESATNGYIEIMFEFDRIRNFTTMKVHCNNMFAKVKIFK	300
251	WPGYDVYGVWRNESATNGYIEIMFEFDRIRNFTTMKVHCNNMFAKVKIFK	300

FIG. 14

```

301 EVQCYRSEASEWEPNAISFPLVLDVNP SARFVTVPLHHRMASAIKQY 350
|||||
301 EVQCYRSEASEWEPNAISFPLVLDVNP SARFVTVPLHHRMASAIKQY 350
|||||
351 HFADTWMFSEITFQSDAAMYNNSALPTSPMAPTYDPM LKVDDSNTRI 400
|||||
351 HFADTWMFSEITFQSDAAMYNNSALPTSPMAPTYDPM LKVDDSNTRI 400
|||||
401 LIGCLVAIIFILLAIIVILWRQFWQKMLEKASRRMLDDEMTVSLSPSD 450
|||||
401 LIGCLVAIIFILLAIIVILWRQFWQKMLEKASRRMLDDEMTVSLSPSD 450
|||||
451 SSMFNRRSSSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGEEE 500
|||||
451 SSMFNRRSSSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGEEE 500
|||||
501 SG.....EDDVVE.QGVKGETSASI 519
|| | |: | | | |: | :
501 SGCSGVVKVPQPSGPEGVPHYAEADIVNLQGV TGGNTYSV 540

```

FIG. 14 (CONT.)¹

```

1 MANFQEHLSGSSPHLPFSEKTFNGLQDELTA MGNHPSPKLLEDQOEKG 50
|||||
1 MANFQEHLSGSSPHLPFSEKTFNGLQDELTA MGNHPSPKLLEDQOEKG 50
|||||
51 MVRTELIESVHSPVTTVLT SVSEDSRDQFENSVLQREHDESETAVSQG 100
|||||
51 MVRTELIESVHSPVTTVLT SVSEDSRDQFENSVLQREHDESETAVSQG 100
|||||
101 NSNTVDGESTGTE DIKIQFSRSGSGGFLEGLFGCLRPVWNII GKAYS 150
|||||
101 NSNTVDGESTGTE DIKIQFSRSGSGGFLEGLFGCLRPVWNII GKAYS 150
|||||
151 TDYKFMQQDTWEVPFEEISELQWLGSAQGA VFLGKFRAE EVAIKK VREQ 200
||||:|||||
151 TDYKLQQQDTWEVPFEEISELQWLGSAQGA VFLGKFRAE EVAIKK VREQ 200
|||||
201 NETDIKHLRLKHPNIIAFKGVCTQAPCYCI IMEYCAHGQLYEVLRA GRK 250
|||||
201 NETDIKHLRLKHPNIIAFKGVCTQAPCYCI IMEYCAHGQLYEVLRA GRK 250
|||||
251 ITPRLLDVWSTGIASGMNYLHLHKI IHRDLKSP 283
|||||
251 ITPRLLDVWSTGIASGMNYLHLHKI IHRDLKSP 283

```

FIG. 15

```

21 KSGNKS VHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 70
  ::|||||
295 EGNKSVHLRKASSPNLHRRQWEKNVPNTALTALENASILTSSLTAEDDR 344
      .
71 GGSVIKYSKNTRKQWLKETPD TLLNLIKKNADLSIAFQTYTYIRPGSEGF 120
  |||||
345 GGSVIKYSKNTRKQWLKETPD TLLNLIKKNADLSIAFQTYTYIRPGSEGF 394
      .
121 LKGP LSEETEASDSDVGGHDSVILDPERLEPGLDEEDTDFEEEDDNPDPWV 170
  |||||
395 LKGP LSEETEASDSDVGGHDSVILDPERLEPGLDEEDTDFEEEDDNPDPWV 444
      .
171 SELKKRAGWQGLCDR 185
  |||||
445 SELKKRAGWQGLCDR 459

```

FIG. 16

1 MAPPSEETPLIPQRCSLLSTEAGALHVLLPARGPGPPQRLSFSFG 46
|||||
1 MAPPSEETPLIPQRCSLLSTEAGALHVLLPARAGPPQRLSFSFG 46

FIG. 17

```

1 MAESACASSFFPLVLLLAGSGGPRGVQALLCACTSCLOANYTCETDG 50
  |||||
1 MAESACASSFFPLVLLLAGSGGPRGVQALLCACTSCLOANYTCETDG 50
  |||||
51 ACMVSI FNLDGMEHHVRTCIPKVELVPAGKPFYCLSS EDLRNTHCCYTDY 100
  |||||
51 ACMVSI FNLDGMEHHVRTCIPKVELVPAGKPFYCLSS EDLRNTHCCYTDY 100
  |||||
101 CNRIDLRVPSGHLKEPEHPSMMWGPVELVGIIAGPVFLFLIIIVFLVIN 150
  |||||
101 CNRIDLRVPSGHLKEPEHPSMMWGPVELVGIIAGPVFLFLIIIVFLVIN 150
  |||||
151 YHQRVYHNQRQLMEDPSC EMCLSKDKTLQDLVYDLSTSGSGSGTKFF 198
  |||||
151 YHQRVYHNQRQLMEDPSC EMCLSKDKTLQDLVYDLSTSGSGSGGLPLF 198
  |||||

```

FIG. 18

[illegible]

FIG. 19

```

251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRTTFPRIR 300
    |||||
251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRTTFPRIR 300
    |||||
301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRRLRSADSENALSVQERN 350
    |||||
301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRRLRSADSENALSVQERN 350
    |||||
351 VPTKCEELSLAPRRRLPRWSQTSYGGKQLG 379
    ||| : ||
351 VPTKSPSAPINWRR.....GKLLG 369

```

FIG. 19 (CONT.¹)

```

1 MDEQFALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQKKHNSSSS 50
  |||||
1 MDEQFALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQ..... 42
  |||||

51 ALLNSPTVTSSCAGASEKKKFLSDVRIKFEHNGERRIIAFSRPVKYEDV 100
  |||||
43 .....SDVRIKFEHNGERRIIAFSRPVKYEDV 69
  |||||

101 EHKVTTVFGQPLDLHYMNNELSILLKNQDDLDKAIDILDRSSSMKSIRIL 150
  |||||
70 EHKVTTVFGQPLDLHYMNNELSILLKNQDDLDKAIDILDRSSSMKSIRIL 119
  |||||

151 LLSQDRNHNSSSPHSEVSRQVRIKASQAGDINTIYQPEPRSRHLSVSS 200
  |||||
120 LLSQDRNHNSSSPHSEVSRQVRIKASQAGDINTIYQPEPRSRHLSVSS 169
  |||||

201 QNPGRSSPPPGYVPERQQHIARQGSYTSINSEGEFIPETSEQCMLDPLSS 250
  |||||
170 QNPGRSSPPPGYVPERQQHIARQGSYTSINSEGEFIPETSEQCMLDPLSS 219
  |||||

```

FIG. 20

```

251 AENSLGSCQSLDRSADSPSFRKSRMSRAQSFDPNQRQEYSDRETQLYDKG 300
    |||||
220 AENSLGSCQSLDRSADSPSFRKSRMSRAQSFDPNQRQEYSDRETQLYDKG 269
    |||||
301 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSRSLSLSTNG 350
    |||||
270 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSRSLSLSTNG 319
    |||||
351 ENMGLAVQYLDPRGRLRSADSENALSVQERNVPTKCEELSLARRRLPRWS 400
    |||||
320 ENMGLAVQYLDPRGRLRSADSENALSVQERNVPTKSPSAPINWRR..... 364
    || ||
    365 .....GKLLG 369

```

FIG. 20 (CONT.¹)

1 MAKQDSVECPFCDEVSKYEKLAIGQTFGEVFKARHRTGQKVALKKV 50
 |||||
 1 MAKQDSVECPFCDEVSKYEKLAIGQTFGEVFKARHRTGQKVALKKV 50
 51 LMENEKEGFPITALREIKIQLLKHENVVNLIEICRTKASPNRCKGSIY 100
 |||||
 51 LMENEKEGFPITALREIKIQLLKHENVVNLIEICRTKASPNRCKGSIY 100
 101 LVDFCEHDLAGLLSNVLVKFTLSEIKRVMQMLNGLIYY..... 139
 |||||
 101 LVDFCEHDLAGLLSNVLVKFTLSEIKRVMQMLNGLIYYIHRNKILHRDM 150
 139 139
 151 KAANVLITRDGVIKLADFLGLARAFSLAKNSQPNRYTNRVVTLWYRPPPELL 200
 139
 201 LGERDYGPIDLWGAGCIMAEMWTRSPIMQNGTEQHQALALISQLCGSITP 250

FIG. 21

139 139
 251 EVWPNVDNYELYEKLELVKGQKRKVKDRPKAYVRDPYALDLIDKLLVLDP 300
 140NHDFWSDPMPSDLKGMSTHLTSMFEYLAPPRKGSQIT 179
 |||||.....
 301 AQRIDDDALNHDFWSDPMPSDLKGMSTHLTSMFEYLAPPRKGSQIT 350
 180 QOSTNQSRNPATTNQTEFERVF 201
 |||||.....
 351 QOSTNQSRNPATTNQTEFERVF 372

FIG. 21 (CONT.¹)

```

1 MATSRYEPVAEIGVAYGTVYKARDPHSGHFCALKSVRVPNGGGGGGGLP 50
  |||||
1 MATSRYEPVAEIGVAYGTVYKARDPHSGHFVALKSVRVPNGGGGGGGLP 50
  |||||
51 ISTVREVALRRLEAFEHPNVVRLMDVCATSRDREIKVTLVFEHVDQDL 100
  |||||
51 ISTVREVALRRLEAFEHPNVVRLMDVCATSRDREIKVTLVFEHVDQDL 100
  |||||
101 RTYLDKAPPPGLPAETIK 118
  |||||
101 RTYLDKAPPPGLPAETIK 118
  |||||

```

FIG. 22

1 MATSRYPVAEIGVGAYGTVVKARDPHSGHFCALKSVRP 40
 |||||
 1 MATSRYPVAEIGVGAYGTVVKARDPHSGHFVALKSVRP 40

FIG. 23

FIG. 24

```

28 LLSPSGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 77
   :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 LDDYGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 367

       .      .      .      .      .      .      .      .
78 YWGLGCLIIYEMIEGQSPFRGRKEKVKREEDRVLETEEVYSHKFSEEAK 127
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
368 YWGLGCLIIYEMIEGQSPFRGRKEKVKREEDRVLETEEVYSHKFSEEAK 417

       .      .      .      .      .      .      .      .
128 SICKMLLTDKAQRLGCQEEGAEEVKRHPFFRNMFKRLEAGMLDPPFVP 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
418 SICKMLLTDKAQRLGCQEEGAEEVKRHPFFRNMFKRLEAGMLDPPFVP 467

       .      .      .      .      .      .      .      .
178 DPAVYCKDVLDIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPQNEMIE 227
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
468 DPAVYCKDVLDIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPQNEMIE 517

       .      .      .      .      .      .      .      .
228 TECFKELNVFGPNGTLPDDLNRNHPPEPPKKGLLQRLFKRHQNNKSASP 277
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
518 TECFKELNVFGPNGTLPDDLNRNHPPEPPKKGLLQRLFKRHQNNKSASP 567

           .      .      .      .      .      .      .      .
278 SSKTSFNHHHINSNHVSSNSTGSS 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
568 SSKTSFNHHHINSNHVSSNSTGSS 590

```

FIG. 25

1 MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50
 |||||
 1 MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50
 |||||
 51 MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPSEVTGVSVLAERCKKNNG 100
 |||||
 51 MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPSEVTGVSVLAERCKKNNG 100
 |||||
 101 KAEFWLDLQPOAKVIMSVQYFLEDVCKQSMRSEDEAKFPTMRRGAIKQ 150
 |||||
 101 KAEFWLDLQPOAKVIMSVQYFLEDVCKQSMRSEDEAKFPTMRRGAIKQ 150
 |||||
 151 AKIHYIKNHEFIATFFGQPTFCQSVCKDFVWGLNKQGYKCRQCNAAIHKKC 200
 |||||
 151 AKIHYIKNHEFIATFFGQPTFCQSVCKDFVWGLNKQGYKCRQCNAAIHKKC 200
 |||||
 201 IDKIIGRCTGTAANSRDTIFQKERFNDMPHRFKVHNYMSPTFCDHCGSL 250
 |||||
 201 IDKIIGRCTGTAANSRDTIFQKERFNDMPHRFKVHNYMSPTFCDHCGSL 250
 |||||
 251 LLPAPHDKHQW.....DCG 264
 |
 251 L.....WGLVKQLKCEDCG 265
 |||

FIG. 27

```

1 MDETHPGYKEVDLEFLVSPSLPCLLSFAGSARHLVPPDSNLFSKLWACG 50
  |||||
203 MDETHPGYKEVD.....LWACG 220

51 VILFTLLAGSPFWHRRQILMLRMIMEGYQFSSPEWDDRSSTVKDLISR 100
  |||||
221 VILFTLLAGSPFWHRRQILMLRMIMEGYQFSSPEWDDRSSTVKDLISR 270

101 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQFRVAVWTVLAAGR 150
  |||||
271 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQFRVAVWTVLAAGR 320

151 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWKKGEOQNR 200
  |||||
321 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWKKGEOQNR 370

201 AALFQHRPPGPFIMGPEEGDSAAITEDEAVILVG 236
  |||||
371 AALFQHRPPGPFIMGPEEGDSAAITEDEAVILVG 406

```

FIG. 28

1 MAFCAMRSSKKTEVNLEAPEGVEVIFYLSREPLRLGSGEYTAELCI 50
 |||||
 1 MAFCAMRSSKKTEVNLEAPEGVEVIFYLSREPLRLGSGEYTAELCI 50
 |||||
 51 RAAQACRISPLCHNLFALYDENTKLWYAPNRTITVDDKMSRLHYRMFY 100
 |||||
 51 RAAQACRISPLCHNLFALYDENTKLWYAPNRTITVDDKMSRLHYRMFY 100
 |||||
 101 FTNWHGTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG 150
 |||||
 101 FTNWHGTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG 150
 |||||
 151 QYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMMKMQLPELP 200
 |||||
 151 QYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMMKMQLPELP 200
 |||||
 201 KDISYKRYIPETLNKSIQRNLLTRMRINNVEKDFLKEFNKTCIDSSVS 250
 |||||
 201 KDISYKRYIPETLNKSIQRNLLTRMRINNVEKDFLKEFNKTCIDSSVS 250
 |||||
 251 THDLVKVYLATLETITKHYGAEIFETSMLLISSENMNWFHSDGGNVLY 300
 |||||
 251 THDLVKVYLATLETITKHYGAEIFETSMLLISSENMNWFHSDGGNVLY 300

FIG. 29

```

301 YEVVMTGNLGIQWRHKPNVVSVEKEKNKLRKKLENKDKKDEEKNKIREE 350
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 YEVVMTGNLGIQWRHKPNVVSVEKEKNKLRKKLENKDKKDEEKNKIREE 350

351 WNNFSFFPEITHIVIKESVVSINKQDNKKMELKLSHSEEALESFVSLVDGY 400
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 WNNFSFFPEITHIVIKESVVSINKQDNKKMELKLSHSEEALESFVSLVDGY 400

401 FRLTADAHHYLCTDVAPPLIVHNIQNGCHGPICTEYAINKLREQEGSEGM 450
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
401 FRLTADAHHYLCTDVAPPLIVHNIQNGCHGPICTEYAINKLREQEGSEGM 450

451 YVLRWCTDFDNIIMTVTCFEKSEQVQGAQKQFNFIQEVQKGYSYLHGS 500
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
451 YVLRWCTDFDNIIMTVTCFEKSEQVQGAQKQFNFIQEVQKGYSYLHGS 500

501 DRSFPSLGDMLSHLKKQILRTDNISFMLKRCQPKPR 537
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501 DRSFPSLGDMLSHLKKQILRTDNISFMLKRCQPKPR 537

```

FIG. 29 (CONT.¹)

```

1  MGCVCCKKEATKLT EERDGS LNQSSGYRYGTDPTPQHYP SFGVTSIPNY 50
   |||||
1  MGCVCCKKEATKLT EERDGS LNQSSGYRYGTDPTPQHYP SFGVTSIPNY 50
   |||||
51 NNFAAGGQGLTV FGGVNSSSHTGTLTRGGTGVTLFVALYDYEARTEDD 100
   |||||
51 NNFAAGGQGLTV FGGVNSSSHTGTLTRGGTGVTLFVALYDYEARTEDD 100
   |||||
101 LSFHKGEKFQIL NSSEGDWWWEARSLTTGETGYIPSNYVAPVDSIQAE EY 150
   |||||
101 LSFHKGEKFQIL NSSEGDWWWEARSLTTGETGYIPSNYVAPVDSIQAE EY 150
   |||||
151 FGKLGKDAERQ LLSFGNPRGTF LIRES ETTKGAYSLSIRDWDDMKGDHV 200
   |||||
151 FGKLGKDAERQ LLSFGNPRGTF LIRES ETTKGYSLSIRDWDDMKGDHV 200
   |||||
201 KHYKIRKLDNGG YIITTRAQFETLQQLVQHYSERAAGLCCRLVVPCHKGM 250
   |||||
201 KHYKIRKLDNGG YIITTRAQFETLQQLVQHYSERAAGLCCRLVVPCHKGM 250
   |||||
251 PRLTDL SVKTKDVWEIPRESIQ LIKRLNGQFGEVWWMG 288
   |||||
251 PRLTDL SVKTKDVWEIPRESIQ LIKRLNGQFGEVWWMG 288

```

FIG. 30

```

1  MGCVCCKEATKLTEERDGLNQSSGYRYGTDTPQHYPFSGVTSIPNY 50
   |||||
1  MGCVCCKEATKLTEERDGLNQSSGYRYGTDTPQHYPFSGVTSIPNY 50
   |||||
51  NNFHAAGGQGLTVFGGVNSSHTGTLRTRGGTGVTLFVALYDYEARTEDD 100
   |||||
51  NNFHAAGGQGLTVFGGVNSSHTGTLRTRGGTGVTLFVALYDYEARTEDD 100
   |||||
101 LSFHKGEKFFQILNSSEGDWEARSLTTGETGYTPSNYVAPVDSIQAEWY 150
   |||||
101 LSFHKGEKFFQILNSSEGDWEARSLTTGETGYTPSNYVAPVDSIQAEWY 150
   |||||
151 FGKLGKDAERQLLSFGNPRGTFLIRESSETTKGAYSLSIRDWDDMKGDHV 200
   |||||
151 FGKLGKDAERQLLSFGNPRGTFLIRESSETTKGAYSLSIRDWDDMKGDHV 200
   |||||
201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
   |||||
201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
   |||||

```

FIG. 31

251 PRLDLSVKT KDWEI PRES LQLIKRLGNGQFGEVMMGTWNGNTKVAIKT 300
 |||||
 251 PRLDLSVKT KDWEI PRES LQLIKRLGNGQFGEVMMGTWNGNTKVAIKT 300
 |||||
 301 LKPGTMSPE SFLEEAQIMKKLKHDKLVQLYAVVSEEPYIVTEYMNKG 348
 |||||
 301 LKPGTMSPE SFLEEAQIMKKLKHDKLVQLYAVVSEEPYIVTEYMNKG 348

FIG. 31 (CONT.¹)

50 SLELHKRRKALTEPEARYYLQIVLGCQYLHNRNVIHRDLKLGNLFLNE 99
 |||
 137 SLELHKRRKALTEPEARYYLQIVLGCQYLHNRNVIHRDLKLGNLFLNE 186
 |||
 100 DLEVKIGDFGLATKVEYDGERKKTLCGTPNYIAPEVLSKKGHSFEVDVWS 149
 |||
 187 DLEVKIGDFGLATKVEYDGERKKTLCGTPNYIAPEVLSKKGHSFEVDVWS 236
 |||
 150 IGCIMYTLLVGKPPFETSLKETYLRIKKNEYSIPKHINPVAASLIQKML 199
 |||
 237 IGCIMYTLLVGKPPFETSLKETYLRIKKNEYSIPKHINPVAASLIQKML 286
 |||
 200 QTDTARPTINELLNDEFTSGYIPARLPITCLTIPPRFSIAPSSLDPSN 249
 |||
 287 QTDTARPTINELLNDEFTSGYIPARLPITCLTIPPRFSIAPSSLDPSN 336
 |||
 250 RKPLTVLNKGLENPLPERPREKEEPVVRETGEVVDCHLSDMLQQLHSVNA 299
 |||
 337 RKPLTVLNKGLENPLPERPREKEEPVVRETGEVVDCHLSDMLQQLHSVNA 386
 |||

FIG. 32

```

300 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSKYGLGYQLCDNSVGVL 349
|||||
387 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSKYGLGYQLCDNSVGVL 436
|||||
350 NDSTRLLYNDGDSLQYIERDGTESYLTVSSHPNSLMKKITLLKYFRNYM 399
|||||
437 NDSTRLLYNDGDSLQYIERDGTESYLTVSSHPNSLMKKITLLKYFRNYM 486
|||||
400 SEHLKAGANITPREGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 449
|||||:|||||
487 SEHLKAGGNITPRQGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 536
|||||
450 DHTKLIPLMAAVTYIDEKRDFTYRLSLLEEYGCCKELASRLRYARTM 499
|||||
537 DHTKLIPLMAAVTYIDEKRDFTYRLSLLEEYGCCKELASRLRYARTM 586
|||||
500 VDKLLSSRSASNRLKAS 516
|||||
587 VDKLLSSRSASNRLKAS 603

```

FIG. 32 (CONT.¹)

FIG. 33

```

32  ERGLTVAFSILCNTLQPEFSTYLNFCRSRLRFDDKPDYSYLRQLFRNLFHR 81
   |: ::: ||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
230 EKKMSTPIEVLCKGYPSFSTYLNFCRSRLRFDDKPDYSYLRQLFRNLFHR 279

      82  QGFSYDYVFDWNMLKFGASSSSQAQPRD 108
         ||| ||| ||| ||| ||| ||| : ||:
      280 QGFSYDYVFDWNMLKFGAARN...PED 303

```

FIG. 34

```

32  ERGLTVAFSILCNTLQPEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 81
   | : : : : | : | | | | | | | | | | | | | | | | | | | |
230  EKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 279
   . . . . . . . . . . . . . . . . . . . . . . . . . .
82  QGFSYDYVFDWNMLKFG.....GPL.SCQPPALP 109
   | | | | | | | | | | | | | | | | | | | | | | | | | |
280  QGFSYDYVFDWNMLKFGAARNPEDVDRERHEREERMGQLRGSAATRALP 329
   . . . . . . . . . . . . . . . . . . . . . . . . . .
110  CGRPQDELGCSPESRGCGGAARTRTRGEDGAATGVRDPSAPWPETHGGH 159
   | | | | | | | | | | | | | | | | | | | | | | | | |
330  PGPP.....TGATANRLRSAAEPVASTPASRIQPA.....GN 361
   . . . . . . . . . . . . . . . . . . . . . . . . . .
160  CQPAPQCCRRAFGFHASLP.HPAGWQYFSQSDIAGR 193
   : | | | | : | : | : | : | : | : | : | : | : |
362  TSPRAISRVDREKVMRLHRGAPANVSSSDLTGR 396

```

FIG. 35

167 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPPELPGGDDLKS 216
 1 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPPELPGGDDLKS 50

217 PEEKKTATQLHSKRRPK 233
 51 PEEKKTATQLHSKRRPK 67

FIG. 36

```

1  MSAKVRILKKLEQLLLDGPWRNESALS VETLLDVLVCLYTECSHSALRRDK 50
  |||
1  MSAKVRILKKLEQLLLDGPWRNESALS VETLLDVLVCLYTECSHSALRRDK 50
  |||
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEI IKVIGRGAFGEVAVVKMKNTER 100
  |||
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEI IKVIGRGAFGEVAVVKMKNTER 100
  |||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||
151 LVMDYVVGDDLTLTLLSKFEDKLPEDMARFYIGEMVLAI DSIHQLHYVHRD 200
  |||
151 LVMDYVVGDDLTLTLLSKFEDKLPEDMARFYIGEMVLAI DSIHQLHYVHRD 200
  |||
201 IKPDNVLLDVNGHIRLADEGSLKMNDGT VQSSVAVGTPDYISPEILQA 250
  |||
201 IKPDNVLLDVNGHIRLADEGSLKMNDGT VQSSVAVGTPDYISPEILQA 250
  |||

```

FIG. 37

```

251 MEDGMGKYGPECDWWSLGVCMYEMLYGETPFYAESLIVETYGKIMNHEERF 300
    |||||
251 MEDGMGKYGPECDWWSLGVCMYEMLYGETPFYAESLIVETYGKIMNHEERF 300
    |||||

301 QFPSHVTDVSEEAkdLIQRlSC 322
    |||||
301 QFPSHVTDVSEEAkdLIQRlLC 322
    |||||

```

FIG. 37 (CONT.¹)

```

1  MSKVRLLKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECHSALRRDK 50
  |||||
1  MSKVRLLKLEQLLLDGPWRNESALSVEITLLDVLVCLYTECHSALRRDK 50
  |||||
51 YVAEFLEWAKPTQLVKEMQLHREDFEI IKVIGRGAFGEVAVVMKNTER 100
  |||||
51 YVAEFLEWAKPTQLVKEMQLHREDFEI IKVIGRGAFGEVAVVMKNTER 100
  |||||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||||
151 LVMDYVVGDDLTLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRD 200
  |||||
151 LVMDYVVGDDLTLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRD 200
  |||||
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231
  |||||
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231

```

FIG. 38

```

1 MELRVGNRYRLGRKIGSGSFGDIYL..... 25
  |||||
1 MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLH 50
26 .....VGIPTRWCGAEGDYNVMVMELLGPSLEDLNFNFCSRKF 63
  |||||
51 IESKIYKMQGGVGIPTRWCGAEGDYNVMVMELLGPSLEDLNFNFCSRKF 100
64 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFMGLGKKGNLVYIIDF 113
  |||||
101 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFMGLGKKGNLVYIIDF 150
114 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLESIG 163
  |||||
151 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLESIG 200
164 YVIMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 213
  |||||
201 YVIMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 250

```

FIG. 39

708 周 明

FIG. 39 (CONT.¹)

```

14 TFAAPSFDDKILEVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 63
|||||
817 TFAAPSFDDKILEVAVFGSMQMAVSRVIRLQHHRIAQCRTVKISILGDE 866
|||||
64 GVPVQVDGEAWVQPPGYIRIVHKNRAQTILTRDRAFESTLKSWEDKQKCEL 113
|||||
867 GVPVQVDGEAWVQPPGYIRIVHKNRAQTILTRDRAFESTLKSWEDKQKCEV 916
|||||
114 PRPSCSLHPPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDMQEOLA 163
|||||
917 PRPSCSLHPPEMLSEEEATQMDQFGQAAGVLIHSIREIAQSHRDMQEOLA 966
|||||
164 HAVNASSKSMDRVYGKPRTEGLNCFSVLEMVNNFRALRSETELLSGKM 213
|||||
967 HAVNASSKSMDRVYGKPRTEGLNCFSVLEMVNNFRALRSETE.LLSGKM 1015
|||||
214 ALQLDPPQKEQLGSALAEMDRQLRRLADTPWLCQSAEPGDEESVMLDLAK 263
|||||
1016 ALQLDPPQKEQLGSALAEMDRQLRRLADTPWLCQSAEPGDEESVMLDLAK 1065
|||||

```

FIG. 40

264 RSRSGKFRFLVTKFKKKNKKEAHSSLGAPVHLWGTEEVAAWLEHLSL 313
 |||||
 1066 RSRSGKFRFLVTKFKKKNKKEAHSSLGAPVHLWGTEEVAAWLEHLSL 1115
 |||||
 314 EYKDIFTRHDIRGSELLHLERRDLKDLGVTKVGHMKRILCGIKELSRSA 363
 |||||
 1116 EYKDIFTRHDIRGSELLHLERRDLKDLGVTKVGHMKRILCGIKELSRSA 1165
 |||||
 364 AVEA 367
 |||||
 1166 AVEA 1169

FIG. 40 (CONT.¹)

```

1 MSDVAIVKEGWLHKGGEYIKTWPRPYFLLKNDGTFIGYKERPOVDQREA 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MSDVAIVKEGWLHKGGEYIKTWPRPYFLLKNDGTFIGYKERPOVDQREA 50
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 PLNFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVETPEEREWT 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 PLNFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVETPEEREWT 100
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 TAIQTVADGLKKQEEEEEMDFRSGSPSDNSGAEEEMVSLAKPKHRVAL 147
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 TAIQTVADGLKKQEEEEEMDFRSGSPSDNSGAEEEMVSLAKPKHRVTM 147
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

FIG. 41

1 MIVHDDVESEPA MTPSKEGTLIVRQTQSASSTLQKHKSSSFTPFIDPRL 50
 |||||
 751 MIVHDDVESEPA MTPSKEGTLIVRQTQSASSTLQKHKSSSFTPFIDPRL 800
 |||||
 51 LQISPSSGTTVTSVVGFSCDGM RPEAIRQDPTRKGSVVNVNPTNTRPQSD 100
 |||||
 801 LQISPSSGTTVTSVVGFSCDGM RPEAIRQDPTRKGSVVNVNPTNTRPQSD 850
 |||||
 101 TPEIRKYKRRFNSEILCAALWGYNLLVGTESGLMLLDRSGQGVYPLINR 150
 |||||
 851 TPEIRKYKRRFNSEILCAALWGYNLLVGTESGLMLLDRSGQGVYPLINR 900
 |||||
 151 RRFAQMDVLEGLNVLTISGKKDKLRVYILSWLRNKILHNDPEVEKKQGW 200
 |||||
 901 RRFAQMDVLEGLNVLTISGKKDKLRVYILSWLRNKILHNDPEVEKKQGW 950
 |||||
 201 TTVDGLEGCVHYKVKYERIKFLVIALKSSVEVYAWAPKPYHKFMFKSF 250
 |||||
 951 TTVDGLEGCVHYKVKYERIKFLVIALKSSVEVYAWAPKPYHKFMFKSF 1000
 |||||

FIG. 42

```

251  GELVHKPLLVDLTVEEGQRLKVIYGSACGFHAVDSDSGSVYDIYLPTHIQ 300
    |||||
1001 GELVHKPLLVDLTVEEGQRLKVIYGSACGFHAVDSDSGSVYDIYLPTHIQ 1050
    |||||

301  CSIKPHAIILPNTDGMELLVCYEDEGVVNTYGRITKDVVLQWGEPTS 350
    |||||
1051 CSIKPHAIILPNTDGMELLVCYEDEGVVNTYGRITKDVVLQWGEPTS 1100
    |||||

351  VAYIRSNQTMGWGEKAIEIRSVETGHLDGVFMHKRAQRLKFLCERNDKVF 400
    |||||
1101 VAYIRSNQTMGWGEKAIEIRSVETGHLDGVFMHKRAQRLKFLCERNDKVF 1150
    |||||

    401 FASVRSGGSQVYFMTLGRTSLSW 425
        |||||
    1151 FASVRSGGSQVYFMTLGRTSLSW 1175

```

FIG. 42 (CONT.¹)

14 GEVDLTALAKELRAVEDVRPHKVTDYSSSESGTTDEEDDDVEQEGAD 63
 |||||
 674 GEVDLTALAKELRAVEDVRPHKVTDYSSSESGTTDEEDDDVEQEGAD 723
 |||||
 64 ESTSGPEDTRAASSNLNSGETESVKTMIVHDDVESEPA MTPSKEGTLIV 113
 |||||
 724 ESTSGPEDTRAASSNLNSGETESVKTMIVHDDVESEPA MTPSKEGTLIV 773
 |||||
 114 RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR 163
 |||||
 774 RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR 823
 |||||
 164 PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV 213
 |||||
 824 PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV 873
 |||||
 214 NLLVGTESGLMLLDRSGQGVYPLINRRRRFQQMDVLEGLNVLV TISGKKD 263
 |||||
 874 NLLVGTESGLMLLDRSGQGVYPLINRRRRFQQMDVLEGLNVLV TISGKKD 923
 |||||
 264 KLRVYLSWLNRKILHNDPEVEKKQGWTTVGDLEGCVHYKVVKYERIKFL 313
 |||||
 924 KLRVYLSWLNRKILHNDPEVEKKQGWTTVGDLEGCVHYKVVKYERIKFL 973
 |||||

FIG. 43

314	VIALKSSVEVYAWAPKPYHKFMFKSFGELVHKPLLDLTVEEGQRLKVI	363
974	VIALKSSVEVYAWAPKPYHKFMFKSFGELVHKPLLDLTVEEGQRLKVI	1023
364	YGSCAGFHAVDVGSGVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCY	413
1024	YGSCAGFHAVDVGSGVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCY	1073
414	EDEGVYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSV	463
1074	EDEGVYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSV	1123
464	TGHLDGVMHKRAQRLKFLCERNDKVFFASVRSQVYFMTLGRSLL	513
1124	TGHLDGVMHKRAQRLKFLCERNDKVFFASVRSQVYFMTLGRSLL	1173
	514 SW 515	
	1174 SW 1175	

FIG. 43 (CONT.)¹

FIG. 44

314	KVIYGSCAGFHAVDVGSGVYDIYLP	THIQCSIKPHAIILPNTDGMELL	363
1021	KVIYGSCAGFHAVDVGSGVYDIYLP	THIQCSIKPHAIILPNTDGMELL	1070
364	VCYEDEGVYVNTYGRITKDVVLQW	GEMPTSVAYIRSNQTMGWGEKAIEIR	413
1071	VCYEDEGVYVNTYGRITKDVVLQW	GEMPTSVAYIRSNQTMGWGEKAIEIR	1120
414	SVETGHLDGVMHKRAQRLKFLCERN	DKVFASVRSGGSSQVYFMTLGR	463
1121	SVETGHLDGVMHKRAQRLKFLCERN	DKVFASVRSGGSSQVYFMTLGR	1170
	464	SLLSW	468
	1171	SLLSW	1175

FIG. 44 (CONT.¹)

```

1 MDCQLSILLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWISYPSH 50
  |||||
1 MDCQLSILLSCSVLDSFGELIPQPSNEVNLLDSKTIQELGWISYPSH 50
  |||||
51 GWEEISGVDEHYTPIRTYQVCNVMDHSONNWLRTNWVPRNSAQKIYVELK 100
  |||||
51 GWEEISGVDEHYTPIRTYQVCNVMDHSONNWLRTNWVPRNSAQKIYVELK 100
  |||||
101 FTLRDCNSIPLVLGTCKETFNLIYMESDDDDHGVKFREQHTKIDTIAADE 150
  |||||
101 FTLRDCNSIPLVLGTCKETFNLIYMESDDDDHGVKFREQHTKIDTIAADE 150
  |||||
151 SFTQMDLGDRILKLNTEIREVGPVNKKGFYLAQDVGCACVALSVRVYFK 200
  |||||
151 SFTQMDLGDRILKLNTEIREVGPVNKKGFYLAQDVGCACVALSVRVYFK 200
  |||||
201 KCPFTVKNLAMFPDTPVMDSQSLVEVRGSCVNNSEEDPPRMYCSTEGEW 250
  |||||
201 KCPFTVKNLAMFPDTPVMDSQSLVEVRGSCVNNSEEDPPRMYCSTEGEW 250
  |||||

```

FIG. 45

```

251 LVPIGKCSNAGYEERGFMCQACRPGFYKALDGNMKAACPPHSSTQEDG 300
|||||
251 LVPIGKCSNAGYEERGFMCQACRPGFYKALDGNMKAACPPHSSTQEDG 300
|||||

301 SMNCRCENNYFRADKDPSPMACTRPSPSRNVISNINETSIVILDWSWPLD 350
|||||
301 SMNCRCENNYFRADKDPSPMACTRPSPSRNVISNINETSIVILDWSWPLD 350
|||||

351 TGGRKDVTFNIIICKKCGWNIKQCEPCSPNVRFPLPRQFGLTNTTIVTVDLL 400
|||||
351 TGGRKDVTFNIIICKKCGWNIKQCEPCSPNVRFPLPRQFGLTNTTIVTVDLL 400
|||||

401 AHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPVLTIKKDRTSR 450
|||||
401 AHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPVLTIKKDRTSR 450
|||||

451 NSISLSWQEPPEHPNGIILDYEVKYYEKQEQTSTYILRARGTNVTISSLK 500
|||||
451 NSISLSWQEPPEHPNGIILDYEVKYYEKQEQTSTYILRARGTNVTISSLK 500
|||||

```

FIG. 45 (CONT.¹)

```

501 PDIYVFQIRARTAAGYGTNSRKFEFETSPDSESSQVVMIAISAA 550
|||||
501 PDIYVFQIRARTAAGYGTNSRKFEFETSPDSESSQVVMIAISAA 550
|||||
551 VAIILLTVVIYVLIGRFCGYKSKHGADKRLHFGNGHLKLPGLRTYVDPH 600
|||||
551 VAIILLTVVIYVLIGRFCGYKSKHGADKRLHFGNGHLKLPGLRTYVDPH 600
|||||
601 TYEDPTQAVHEFAKELDATNISIDKVVGA 629
|||||
601 TYEDPTQAVHEFAKELDATNISIDKVVGA 629

```

FIG. 45 (CONT.²)

256 KKHFFSGIDWDNIRNCEAPYIPEVSSPTDTSNFDVDDDDCLKNSETMPPP 305
 |||||
 338 KKHFFSGIDWDNIRNCEAPYIPEVSSPTDTSNFDVDDDDCLKNSETMPPP 387
 |||||
 306 THTAFSGHHLPEVGFYTTSSCVLSDRSCLRVTAGPTSLDLDVNVQRTLDN 355
 |||||
 388 THTAFSGHHLPEVGFYTTSSCVLSDRSCLRVTAGPTSLDLDVNVQRTLDN 437
 |||||
 356 NLATEAYERRIKRLEQEKLELSRKLQESTQTVQALQYSTVDGPLTASKDL 405
 |||||
 438 NLATEAYERRIKRLEQEKLELSRKLQESTQTVQALQYSTVDGPLTASKDL 487
 |||||
 406 EIKNLKEEI 414
 |||||
 488 EIKNLKEEI 496

FIG. 46 (CONT.¹)

```

1 MEVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRKRKRAKLIKYL 50
  |||||
1 MEVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRKRKRAKLIKYL 50
  |||||
51 MGDLLGEGSYGKVKVLDSETLCRRRAVKILKKKLLRRIPNGEANVKKEIQ 100
  |||||
51 MGDLLGEGSYGKVKVLDSETLCRRRAVKILKKKLLRRIPNGEANVKKEIQ 100
  |||||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFV 150
  |||||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFV 150
  |||||
151 CQAHG 155
  |||||
151 CQAHG 155

```

FIG. 47

```

1 MEVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLIKYL 50
  |||
1 MEVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLIKYL 50
  |||
51 MGDLLGEGSYGKVKEVLDSETLCRRVVKILKKKLRRIPNGEANVKKEIQ 100
  |||
51 MGDLLGEGSYGKVKEVLDSETLCRRVVKILKKKLRRIPNGEANVKKEIQ 100
  |||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFV 150
  |||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFV 150
  |||
151 CQAHGYFCQLIDGLEYLHSQGIHVHKDIPGNLLLTGGTLKISDLGVAE 199
  |||
151 CQAHGYFCQLIDGLEYLHSQGIHVHKDIPGNLLLTGGTLKISDLGVAE 199
  |||

```

FIG. 48

27 VKDFLSQLRSSNRRESIPESGGTMDGFRTIENQHSRNDVMVSEWLN 76
 |||||:|||||
 301 VKDFLSQLKSSNRRESIPESGGTMDGFRTIENQHSRNDVMVSEWLN 350

 77 KLNLEPPSSVPKKCPSLTKRSRAQEEQVQAWTAGTSSDSMAQPPQTPE 126
 |||||
 351 KLNLEPPSSVPKKCPSLTKRSRAQEEQVQAWTAGTSSDSMAQPPQTPE 400

 127 TSTFRNQMPSPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 176
 |||||
 401 TSTFRNQMPSPSTSTGTPSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 450

 177 NIYNCSGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQHPFPVGSQEGP 226
 |||||
 451 NIYNCSGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQHPFPVGSQEGP 500

 227 KDPEAWSRPQGWYNHSGK 244
 |||||
 501 KDPEAWSRPQGWYNHSGK 518

FIG. 49

```

30 EEQARELYRRLREKPRDQTEGDSQEMVRLLQAIQSFEEKVRVIYQLS 79
   |||||
564 EEQARELYRRLREKPRDQTEGDSQEMVRLLQAIQSFEEKVRVIYQLS 613
   |||||

80 KTVVCKQKALELLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACS 129
   |||||
614 KTVVCKQKALELLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACS 663
   |||||

130 KVRGVPVSGSPDSMNASRLSQPGQLMSQSPSTASNSLPEPAKKEELVAEAEH 179
   |||||
664 KVRGVPVSGSPDSMNASRLSQPGQLMSQSPSTASNSLPEPAKKEELVAEAEH 713
   |||||

180 NLCTLLENAIQDQTVREQDQSFALDWSWLQTEEEHSCLEQAS 222
   |||||
714 NLCTLLENAIQDQTVREQDQSFALDWSWLQTEEEHSCLEQAS 756

```

FIG. 50

```

1 MRLTLLCCTWREERMGEESLPCVASCGRYDGYLQALNADWHADCF 50
|||||
1 MRLTLLCCTWREERMGEESLPCVASCGRYDGYLQALNADWHADCF 50

51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
|||||
51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

101 ELKYHPECFICLTCTGTFIGDGTYYLVEHSLKLYCGHCYYQTVVTPVIEQI 150
|||||
101 ELKYHPECFICLTCTGTFIGDGTYYLVEHSLKLYCGHCYYQTVVTPVIEQI 150

151 LPDSPGSHLPHTVTLVSIPASSHGKRLSVSIDPPHPPGCGTEHSHTVR 200
|||||
151 LPDSPGSHLPHTVTLVSIPASSHGKRLSVSIDPPHPPGCGTEHSHTVR 200

201 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQT SRL 250
|||||
201 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQT SRL 250

```

FIG. 51

251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
|||||
251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVL RSCSID 300
|||||
301 RSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKG GCF 350
|||||
301 RSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKG GCF 350
351 GQAIKV 356
|||||
351 GQAIKV 356

FIG. 51 (CONT.¹)

```

1  MRLLCCTWREERMGESELPVCASCGQRIYDGYLQALNADWHADCF 50
   |||||
1  MRLLCCTWREERMGESELPVCASCGQRIYDGYLQALNADWHADCF 50

51  RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
   |||||
51  RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

101  ELKYHPECFICLTCGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
   |||||
101  ELKYHPECFICLTCGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150

151  LPDSPGSHLPHTVTVLSIPASSHGKRGLSVSDPPHPPGCGTEHSHTVR 200
   |||||
151  LPDSPGSHLPHTVTVLSIPASSHGKRGLSVSDPPHPPGCGTEHSHTVR 200

201  VQGVDPGCMSPDVKNSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
   |||||
201  VQGVDPGCMSPDVKNSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 51

```

251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVLRSCSID 300
|||||
251 QLTLEHDPHDTLGHGLGPETSP LSSPAYTPSGEAGSSARQKPVLRSCSID 300
|||||
301 RSPGAGSLGSPASQKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGCF 350
|||||
301 RSPGAGSLGSPASQKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGCF 350
|||||
351 GQAIKV 356
|||||
351 GQAIKV 356

```

FIG. 51 (CONT.¹)

```

1  MRLTLCCCTWREERMGEESLPCVASCGRYYDQYLQALNADWHADCF 50
  |||||
1  MRLTLCCCTWREERMGEESLPCVASCGRYYDQYLQALNADWHADCF 50
  |||||
51  RCCDCSASLSHQYYEKDGLFCKDYWARYGESCHGCSEQITKGLVMVAG 100
  |||||
51  RCCDCSASLSHQYYEKDGLFCKDYWARYGESCHGCSEQITKGLVMVAG 100
  |||||
101  ELKYHPECFICLTCGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
  |||||
101  ELKYHPECFICLTCGTFIGDGTYYTLVEHSKLYCGHCYYQTVVTPVIEQI 150
  |||||
151  LPDSPGSHLPHTVTLVSPASSHGKRGLSVSDPPHPPGCGTEHSHTVR 200
  |||||
151  LPDSPGSHLPHTVTLVSPASSHGKRGLSVSDPPHPPGCGTEHSHTVR 200
  |||||
201  VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
  |||||
201  VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
  |||||

```

FIG. 52

1	MADAVQSEPRSWLLEQLAGADLAAPGVQQQLELERERURREIRKEL	50
1	MADAVQSEPRSWLLEQLAGADLAAPGVQQQLELERERURREIRKEL	50
51	KLKEGAENLRATTDLGRSLGPVELLLRGSSRRDLLHQQLQELHAHVVL	100
51	KLKEGAENLRATTDLGRSLGPVELLLRGSSRRDLLHQQLQELHAHVVL	100
101	PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVQGAENMIQ	150
101	PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVQGAENMIQ	150
151	TYSNGSTKDKRLLLTAQQMLQDSKTKIDIIRMQLRRALQADOLENQAAAPD	200
151	TYSNGSTKDKRLLLTAQQMLQDSKTKIDIIRMQLRRALQADOLENQAAAPD	200
201	DTQGSFDLGAVELRIEELRHHRFVEHVAEAGAKNVLRLLSAAKAPDRKAV	250
201	DTQGSFDLGAVELRIEELRHHRFVEHVAEAGAKNVLRLLSAAKAPDRKAV	250

FIG. 53

```

251  SEAEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300
      |||
251  SEAEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300
      |||
301  STRLAGPPATHYSTICKPAPLTGTLVVRVVGCRDLPETIPWNPTPSMG 350
      |||
301  STRLAGPPATHYSTICKPAPLTGTLVVRVVGCRDLPETIPWNPTPSMG 350
      |||
351  PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEENTSEVSTVLKLDNT 400
      |||
351  PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEENTSEVSTVLKLDNT 400
      |||
401  VVGQTSWKPCGPNWDQSFTELEERARELELAVFWRDQGLCALKFLKLE 450
      |||
401  VVGQTSWKPCGPNWDQSFTELEERARELELAVFWRDQGLCALKFLKLE 450
      |||
451  DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQKG 500
      |||
451  DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQKG 500
      |||

```

FIG. 53 (CONT.¹)

501	AFQARQMNI	DVATWVRLLRRLIPNATGTGTFSPGASPGSEARTTGD	ISV	550	
501	AFQARQMNI	DVATWVRLLRRLIPNATGTGTFSPGASPGSEARTTGD	ISV	550	
551	EKLNLTDS	DSSPQKSRRDPSSPSLSSIQUESTAPELPSETQETPGPA	600		
551	EKLNLTDS	DSSPQKSRRDPSSPSLSSIQUESTAPELPSETQETPGPA	600		
601	LCSPLRKSP	LTLEDFKFLAVLGRGHFGKVLLSEFRPSGELEFAIKALKKG	D	650	
601	LCSPLRKSP	LTLEDFKFLAVLGRGHFGKVLLSEFRPSGELEFAIKALKKG	D	650	
651	IVARDEVES	IMCEKRILAAVT	SAGHPFLVNLFGCFQTPEHVCFVMEYSAG	700	
651	IVARDEVES	IMCEKRILAAVT	SAGHPFLVNLFGCFQTPEHVCFVMEYSAG	700	
701	GDLMLHIH	SDVFSEPRALFYSA	C.....	723	
701	GDLMLHIH	SDVFSEPRALFYSA	CVLGQLFHEHKIVYRDCLKLDNLLD	T	750

FIG. 53 (CONT.)²

```

723 ..... 723
751 EGYVKIADFLGCKEGMGYGDRTSTFCGTPEFLAPEVLTDTSYTRAVDWMG 800
723 ..... 723
801 LGVLLYEMLVGESPFPGDDEEEVFDSIVNDEVYPRFLSAEAGIMRRL 850
724 .....RLPPFVPTLSGRD 738
      |||||
851 RRNPERLGSSERDAEDVKKQPFRTLGWEALLARLPPPFVPTLSGRD 900
      .
739 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDDFVAGGC 780
      |||||
901 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDDFVAGGC 942

```

FIG. 53 (CONT.)

1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELEFERLRREIRKEL 50
 |||||
 1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELEFERLRREIRKEL 50
 |||||
 51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRDLHLHQQLQELHAHVVL 100
 |||||
 51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRDLHLHQQLQELHAHVVL 100
 |||||
 101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKGAEENMIQ 150
 |||||
 101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKGAEENMIQ 150
 |||||
 151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200
 |||||
 151 TYSNGSTKDRKLLLTAAQMLQDSKTKIDIIRMQLRRALQAGQLENQAAPD 200
 |||||
 201 DTQGSPDLGAVELRIEELRHHFRVEHAVAEGAKNVRLLSAAKAPDRKAV 250
 |||||
 201 DTQGSPDLGAVELRIEELRHHFRVEHAVAEGAKNVRLLSAAKAPDRKAV 250
 |||||

FIG. 54

```

251  SEAEKLTESNQKGLLREALERRIGELPADHPKGRLLREELAAASSAAF 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251  SEAEKLTESNQKGLLREALERRIGELPADHPKGRLLREELAAASSAAF 300

301  STRIAGFPFATHYSTICKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301  STRIAGFPFATHYSTICKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350

351  PGTPDSRPFFLSRPARGLYRSGLSGRSLKAEAEENTSEVSTVILKDNT 400
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351  PGTPDSRPFFLSRPARGLYRSGLSGRSLKAEAEENTSEVSTVILKDNT 400

```

FIG. 54 (CONT.¹)

25 GGRLLCATDVPRTVSSAASQGLHMQNDACLGAASP 62
 403 GEPLYLCATDVPRTVSSAASQGLHMQNDACLGAASP 440

FIG. 55

90 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRLLVKDP 139
 |||||
 211 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRLLVKDP 260
 |||||
 140 KRRMTIAQSLHSHWIKAIRRRNVRGEDSGRKPERRRLKTTTLKEYTIKSH 189
 |||||
 261 KRRMTIAQSLHSHWIKAIRRRNVRGEDSGRKPERRRLKTTTLKEYTIKSH 310
 |||||
 190 SSLPPNNSYADFERFSKVLEEEAAAEGLRELQSRRLCHEDVEALAAIY 239
 |||||
 311 SSLPPNNSYADFERFSKVLEEEAAAEGLRELQSRRLCHEDVEALAAIY 360
 |||||
 240 EEKEAWYREESDSLQDLRRLRQELLKTEALKRQAEAKGALLGTSLK 289
 |||||
 361 EEKEAWYREESDSLQDLRRLRQELLKTEALKRQAEAKGALLGTSLK 410
 |||||
 290 RRFSLRLENRYEALAKQVASEMRFVQDLVRALEQEKLOGVECCGLR 333
 |||||
 411 RRFSLRLENRYEALAKQVASEMRFVQDLVRALEQEKLOGVECCGLR 454

FIG. 56

```

61  GETALHKAACQNRNAVQCQLLVDAGASLRKTDKGTPOERAQQAGDPDLA 110
    |||||
995 GETALHKAACQNRNAVQCQLLVDAGASLRKTDKGTPOERAQQAGDPDLA 1044
    |||||
    111 AYLESRQNYKVIGHEDLETAV 131
    |||||
    1045 AYLESRQNYKVIGHEDLETAV 1065

```

FIG. 57

```

1 MRGAARLGRPRGRCPLPGPAIRAPRPPRLILLIALLPLLAPAGAAAAPR 40
| | | | | | | | | | | | | | : | | | |
1 MRGAARLGRPRGRCPLPGPAIRAAAP..ALLARCAVAAAAGLRAAARPR 48
| | | | | | | | | | | | | | : | | | |

51 PPELQASAGPSVSILYLSDEVRRLIGLDAELYVRNDLISHYALSFLL 100
| | | | | | | | | | | | | | : | | | |
49 PPELQASAGPSVSILYLSDEVRRLIGLDAELYVRNDLISHYALSFNLL 98
| | | | | | | | | | | | | | : | | | |

101 VPSETNFLHTTHAKSKEYKLGQVDNVNLAMDMPQVNISVGGEVPRTL 150
| | | | | | | | | | | | | | : | | | |
99 VPSETNFLHTTHAKSKEYKLGQVDNVNLAMDMPQVNISVGGEVPRTL 148
| | | | | | | | | | | | | | : | | | |

151 VFRVELSCTGKVDSEVMILMQLNLTVNSSKNFTVLNFKRRKMCKKLEEV 200
| | | | | | | | | | | | | | : | | | |
149 VFRVELSCTGKVDSEVMILMQLNLTVNSSKNFTVLNFKRRKMCKKLEEV 198
| | | | | | | | | | | | | | : | | | |

201 KTSALDKNTSRTIYPVHAAPTSTTRVFYISGVCCAVIFLVAIIAHLH 250
| | | | | | | | | | | | | | : | | | |
199 KTSALDKNTSRTIYPVHAAPTSTTRVFYISGVCCAVIFLVAIIAHLH 248
| | | | | | | | | | | | | | : | | | |

251 LHSMKRIELD 261
| | : | | | | | | | |

249 LHNMKRIELD 259

```

FIG. 58

```

1  MPQVNISVQGEVPRTLVSVRVELSCTGKVDSEVMILQNLNTVNSSKNFT 50
   |||||
132 MPQVNISVQGEVPRTLVSVRVELSCTGKVDSEVMILQNLNTVNSSKNFT 181
   |||||
51  VLNFKRRKMCYKKEEVKTSALDKNTSRTIYDPVHAAPTSTRVFIYSVG 100
   |||||
182 VLNFKRRKMCYKKEEVKTSALDKNTSRTIYDPVHAAPTSTRVFIYSVG 231
   |||||
101 VCCAVIFLVAIILAVLHLHSMKRIELDDSISSASSQGLSQPSTQTTQYL 150
   |||||
232 VCCAVIFLVAIILAVLHLHNMKRIELDDSISSASSQGLSQPSTQTTQYL 281
   |||||
151 RADTPNNATPITSSYYPTLRIEKNDLRSVTLLEAKGKVKDIAISRERITL 200
   |||||
282 RADTPNNATPITS..YPTLRIEKNDLRSVTLLEAKGKVKDIAISRERITL 329
   |||||
201 KDVLEQGTGGRIFHGILIDEKDPNKEKQAFVKTVDQDQASEIQVTMMLTES 250
   |||||
330 KDVLEQGTGGRIFHGILIDEKDPNKEKQAFVKTVDQDQASEIQVTMMLTES 379

```

FIG. 59

251 CKLRGLHHRNLLPITHVCIEEGEKPVMILPYMNWGNLKLFLRQCKLVEAN 300
|||||
380 CKLRGLHHRNLLPITHVCIEEGEKPVMILPYMNWGNLKLFLRQCKLVEAN 429
|||||
301 NPQAI SQQDLVHMAIQIACGMSYLAARREVIHKDLAARNCV 340
|||||
430 NPQAI SQQDLVHMAIQIACGMSYLAARREVIHKDLAARNCV 469
|||||

FIG. 59 (CONT.¹)

```

1  MEAIRTDNQNFASQIREAEARNRDLEAHVRQLQERMELLOAEGATAVTGV 50
    |||||
484 MEAIRTDNQNFASQIREAEARNRDLEAHVRQLQERMELLOAEGATAVTGV 533
    .
51  PSPRATDPPSHL.....DGPPAVAVGQCPLVGP.GPMHRRHL 86
    |||||
534 PSPRATDPPSHMAPRPMWLWASARWWGQAPCTAATCCSLPGSLGLAYRR.. 581
    .
87  LLPARVP...RPGLSAELSLLFVVLVSRAAALGCICLVAHAGQLTAVWR 133
    || | |||:| ||| |:: |
582 ...RFPCSCSP.....LFCLVPPPPWAALGWPTPANSPQ..... 612
    134 RPGAARAP 141
        |||: |
        613 .SGAAQEP 619

```

FIG. 60

```

1  MELLQAEGATAVTGVPSPRATDPPSHL.....DGPPAVAVGQ 37
   |||||
519 MELLQAEGATAVTGVPSPRATDPPSHMARPWLWASARWWGQAPCTAATC 568
      |::|:
      |||

38  CPLVGP.GPMHRRHLLPARVP...RPGLSAALSILLFAVLSRAAALGC 83
   | | | | : || | | | | | | | | | | | | | | | | | |
569 CSLPGSLGLAYRR.....RFPCCSP.....LFCLVPPPPWAAALGW 603
      | | | | | | | | | | | | | | | | | | | | | |
      |::| |::| |::| |::| |::| |::| |::| |::| |::|
      84 IGLVAHAGQLTAVWRRPGARAP 106
      604 WPTPANSPO.....SGAAQEP 619

```

FIG. 61

6 HEDFEFISGTRMRKCLAREGQKPPEGFMAPKAWTVLTEYYKSLEKA 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
580 HEDFEFISGTRMRKCLAREGQKPPEGFMAPKAWTVLTEYYKSLEKA 624

FIG. 62

[illegible]

FIG. 63

```

1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLLKTDGSGFIGYKEKPQVDLPYP 50
  |||||
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLLKTDGSGFIGYKEKPQVDLPYP 50
  |||||

51 LNNFSVASSVMFR 63
  |||||: :::
51 LNNFSVAKCQLMK 63

```

FIG. 64

[illegible]

FIG. 65

```

73 SSQYGDRCFMFVLISPTKSVIITILSLFTLQLFFHLSRERVFSEDRTR 122
   | | : | :: : ||||| ||||| |||||
214 SFQTCKDRCLCFVMEYVNGG.....ELFFHLSRERVFSEDRTR 249

123 FYGAIEIVSALDYLHS GKIVYRD LKLENMLDKDGHIKITDFGLCKEGITD 172
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 FYGAIEIVSALDYLHS GKIVYRD LKLENMLDKDGHIKITDFGLCKEGITD 299

173 AATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLLPFYNQ 222
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 AATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLLPFYNQ 349

223 DHEKL FELILMEDIKFPRTLSSDAKSLLSGLLIKDPKNKRLGGGPDDAKEI 272
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350 DHEKL FELILMEDIKFPRTLSSDAKSLLSGLLIKDPKNKRLGGGPDDAKEI 399

273 MRHSFFSGVNWQDVYDKLVPPFKPQVTSETDTRYFDDEEFTAQTITITPP 322
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 MRHSFFSGVNWQDVYDKLVPPFKPQVTSETDTRYFDDEEFTAQTITITPP 449

      323 EKYDEDMCDMNERRPHFPQFSYSASGRE 352
          ||||| ||||| ||||| ||||| |||||
      450 EKYDEDMCDMNERRPHFPQFSYSASGRE 479

```

FIG. 66

```

1 MELLRITYQPAASTKMCQALGKGCGNSKKRPPQPPEESQPPQSQAQ 50
   | | | | | | | | | | | | | | : | | | | | | | | | | | | | |
1 MELLRITYQPAASTKMCQALGKGCGGDSKKRPPQPPEESQPPQSQAQ 50

51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGVLGKGGFAKCYEFT 100
   | | | | | | | | | | | | | | : | | | | | | | | | | | | | |
51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGVLGKGGFAKCYEFT 100

101 DLTNKNKYAAKIIPHRSRVAKPHQREKVCMTLE 132
   | | | | | | | | | | | | | | : |
101 DLTNKNKYAAKIIPHRSRVAKPHQREKIDKEIE 132
```

FIG. 67

```

1 MELLRTITYQPAASTKMCEQALGCGGNSKKRPPQPPEESQPPQSQAQ 50
  |||||
1 MELLRTITYQPAASTKMCEQALGCGGDSKKRPPQPPEESQPPQSQAQ 50
  |||||
51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGGFAKCYEMT 100
  |||||
51 VPPAAPHHHHHSHSGPEISRIIVDPTTGKRYCRGKVLGKGGFAKCYEMT 100
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRIILHHKHVVQFYHYFE 150
  |||||
101 DLTNNKVYAAKIIPHSRVAKPHQREKIDKEIELHRIILHHKHVVQFYHYFE 150
  |||||
151 DKENIYILLEYCSRR..VSVNSYLRTFAYPELTWYSKSLSGI 191
  |||||
151 DKENIYILLEYCSRRSMAHILKARKVLTEPEVRYLRIIVSGL 193

```

FIG. 68

```

1  MELLRTITYQPAASTKMCEQALGKCGGNSKKKRPPQPPEESQPPQSQAQ 50
  |||||
1  MELLRTITYQPAASTKMCEQALGKCGGDSKKKRPPQPPEESQPPQSQAQ 50
  |||||
51 VPPAAPHHHHHHSHSGPEISRRIIVDPTTGKRYCRGKVLGKGGFAKCYEMT 100
  |||||
51 VPPAAPHHHHHHSHSGPEISRRIIVDPTTGKRYCRGKVLGKGGFAKCYEMT 100
  |||||
101 DLTNNKVYAAKIIPHRSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
101 DLTNNKVYAAKIIPHRSRVAKPHQREKIDKEIELHRILHHKHVVQFYHYFE 150
  |||||
151 DKENIYILLEYCSRR 165
  |||||
151 DKENIYILLEYCSRR 165

```

FIG. 69


```

1  MERAI SPGLV RALL LLL LGLAARTVAAGRARGLPAPTAFAAFGLGAAA 50
  |||||
1  MERAI SPGLV RALL LLL LGLAARTVAAGRARGLPAPTAFAAFGLGAAA 50
  |||||
51 APTSATRVPAAGAVAAAEEVTVEDAEALPAAAAGEQEPRGPEPDDTELPR 100
  |||||
51 APTSATRVPAAGAVAAAEEVTVEDAEALPAAAAGEQEPRGPEPDDTELPR 100
  |||||
101 GRSLV IISTLDGRIAALDPENHGKKQWDL DVGSGSLVSSSLSKPEVFGNK 150
  |||||
101 GRSLV IISTLDGRIAALDPENHGKKQWDL DVGSGSLVSSSLSKPEVFGNK 150
  |||||
151 MIIPSLDGALFQWDRDRESMETVPFTVESLLESSYKFGDDVVLVGKSLT 200
  |||||
151 MIIPSLDGALFQWDRDRESMETVPFTVESLLESSYKFGDDVVLVGKSLT 200
  |||||

```

FIG. 71

201 TYGLSAYSGKVRYICSAALGCRQWDSDEMEQEEDILLQRTQKTAVRAGPR 250
 |||||
 201 TYGLSAYSGKVRYICSAALGCRQWDSDEMEQEEDILLQRTQKTAVRAGPR 250
 |||||
 251 SGNEKNFVSGHFELRYIPDMETRAGFIESTFKPNENTEESKII SDVEEQ 300
 |||||
 251 SGNEKNFVSGHFELRYIPDMETRAGFIESTFKPNENTEESKII SDVEEQ 300
 |||||
 301 EAAIMDIVIKVSVADWKVMAFSKKGHLEWEYQFCTPIASAWLLKDGKVI 350
 |||||
 301 EAAIMDIVIKVSVADWKVMAFSKKGHLEWEYQFCTPIASAWLLKDGKVI 350
 |||||
 351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENS VYLGMYRGQLYLQSSV 400
 |||||
 351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENS VYLGMYRGQLYLQSSV 400
 |||||
 401 RISEKFPSPKALESVTNENAIIPLTIKWKPLIHSPSRTPVLVGSDEFD 450
 |||||
 401 RISEKFPSPKALESVTNENAIIPLTIKWKPLIHSPSRTPVLVGSDEFD 450

FIG. 71 (CONT.¹)

```

451 KCLNDKFSHEEYSNGALSILQPYDNGYLYPYKRENRKRSTQITVRL 500
|||||
451 KCLNDKFSHEEYSNGALSILQPYDNGYLYPYKRENRKRSTQITVRL 500
|||||
501 DNPYNNKIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
|||||
501 DNPYNNKIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLFHPPHRQ 550
|||||
551 RKESETQCQTENKYDSVSGEANDSSWNNDIKNSGYISRYLTDFEPIQCLGR 600
|||||
551 RKESETQCQTENKYDSVSGEANDSSWNNDIKNSGYISRYLTDFEPIQCLGR 600
|||||
601 GGFGVVFEAKNKVDDCNAYAIKRIRLPNRELAREKVMREVKALAKLEHPGI 650
|||||
601 GGFGVVFEAKNKVDDCNAYAIKRIRLPNRELAREKVMREVKALAKLEHPGI 650
|||||
651 VRYFNWLEAPPEKWQEKMDIEWLKDESTDWPLSSPSPMDAPSVKIRMD 700
|||||
651 VRYFNWLEAPPEKWQEKMDIEWLKDESTDWPLSSPSPMDAPSVKIRMD 700

```

FIG. 71 (CONT.²)

```

701 PFSTKEHIEIIAPSPQSRSFSGISCDQTSSSESQFSPLEFSGMDHEDI 750
|||||
701 PFSTKEHIEIIAPSPQSRSFSGISCDQTSSSESQFSPLEFSGMDHEDI 750
|||||
751 SESVDAAYNLQDSCLTDCDVEDGTMDGNDEGHSEFELCPSEASPYVRSRER 800
|||||
751 SESVDAAYNLQDSCLTDCDVEDGTMDGNDEGHSEFELCPSEASPYVRSRER 800
|||||
801 TSSSIVFEDSGCDNASSKEEPTNRLHIGNHCANKLT 837
|||||
801 TSSSIVFEDSGCDNASSKEEPTNRLHIGNHCANKLT 837

```

FIG. 71 (CONT.)³

FIG. 72

```

210 . . . . . 210
251 VVLTTPMKMVTTELAPLGSLDLRLKRHQHFLGLTSLRYAVQVAEGMGYLE 300
210 . . . . . 210
301 SKRFTIHRDLAARNLLLATRDLVKIGDFGLMRALPQNDDHYVMQEHKVPF 350
210 . . . . . 210
351 AWCAPESLKTRTFSHASDTWMFGVTIWEMFTYQGEPPWGLNGSQILHKID 400
210 . . . . . 210
401 KEGERLPRPDCPQDIYNVMVQCWAHKPEDRPTFVALRDFLEAQPTDMR 450

```

FIG. 72 (CONT.¹)

348 DDFEICSINSTLVGAGVPAGPSQGQTNYAFVPEQARPPPLEDNLFPPQ 397
 |||||
 698 DDFEICSINSTLVGAGVPAGPSQGQTNYAFVPEQARPPPLEDNLFPPQ 747
 |||||
 398 GGGKPPSSAQTAEIFQALQQECMRQLQAPAGSAPSPGGDDKPQVPPR 447
 |||||
 748 GGGKPPSSAQTAEIFQALQQECMRQLQAP.GSPAPSPGGDDKPQVPPR 796
 |||||
 448 VPIPRPTRPHVQLSPAPPGEEETSQWPGPASPVRVPPREPLSPQGSRT 497
 |||||
 797 VPIPRPTRPHVQLSPAPPGEEETSQWPGPASPVRVPPREPLSPQGSRT 846
 |||||
 498 SPLVPPGSSPLPRLSSSPGKTMTTQSFASDPKYATPQVIQAPGPRAG 547
 |||||
 847 SPLVPPGSSPLPRLSSSPGKTMTTQSFASDPKYATPQVIQAPG.AGGP 895
 |||||
 548 CILPIVRDGKKVSTHYLLPERPSYERYQRFLEAQSPPEEPTPLPVPL 597
 |||||
 896 CILPIVRDGKKVSTHYLLPERPSYERYQRFLEAQSPPEEPTPLPVPL 945

FIG. 72 (CONT.³)

```

598 LLPPPSTPAPAAAPTATVRPMPQAAALDPKANFSTNNSNPGARPPPPRATAR 647
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
946 LLPPPSTPAPAAAPTATVRPMPQAAALDPKANFSTNNSNPGARPPPPRATAR 995
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
648 LPQRCPCGPGPEAGR PADKIQMAMVHGVTTEECQAAALQCHGWSVQACPV 697
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
996 LPQRCPCGPGPEAGR PADKIQMAMVHGVTTEECQAAALQCHGWSVQACPV 1045
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
698 SEGGAALRAGSAAQRECHKVLEMFEDWNLEQAGCHLLGSWGPAHKKR 743
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1046 SEGGAALRAGSAAQRECHKVLEMFEDWNLEQAGCHLLGSWGPAHKKR 1091

```

FIG. 72 (CONT.)⁴

FIG. 73

301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCCDILENVPGRSK 350
 |||||
 301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCCDILENVPGRSK 350
 .
 351 ATSVALPGWSPSETRSSFSMRTSKSGSSRNLLKTDDLSNDVCAVLKLD 400
 |||||
 351 ATSVALPGWSPSETRSSFSMRTSKSGSSRNLLKTDDLSNDVCAVLKLD 400
 .
 401 NTVVGGT¹SWKPISNQSWDQKFTLELDRSRELEISVYWRDWRS¹CAVKFLR 450
 |||||
 401 NTVVGGT¹SWKPISNQSWDQKFTLELDRSRELEISVYWRDWRS¹CAVKFLR 450
 .
 451 LEDFLDNQRHGMCLYLEPQGT¹FAEVTFFNPVIERP¹KLQRQKKIFS¹KQ 500
 |||||
 451 LEDFLDNQRHGMCLYLEPQGT¹FAEVTFFNPVIERP¹KLQRQKKIFS¹KQ 500
 .
 501 GKTF¹LRAPQMNIN¹IATWGRLVRR¹AIPTVNHSGT¹FSPQAPVPT¹VPVVDVR 550
 |||||
 501 GKTF¹LRAPQMNIN¹IATWGRLVRR¹AIPTVNHSGT¹FSPQAPVPT¹VPVVDVR 550
 .
 551 IPQLAPPA 558
 |||||
 551 IPQLAPPA 558

FIG. 73 (CONT.¹)

1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLFSDTMVQQKLLDDIKD 50
 |||||
 1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLFSDTMVQQKLLDDIKD 50
 51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNILKKSNNKLEELHHKL 100
 |||||
 51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNILKKSNNKLEELHHKL 100
 101 QELNAHIVVSDPEDITDCPRTPTPNNDPRCSTSNRLKALQQLDIELK 150
 |||||
 101 QELNAHIVVSDPEDITDCPRTPTPNNDPRCSTSNRLKALQQLDIELK 150
 151 VKQGAENMIQMYSSGSKDRKLHGTAQQLLQDSKTKIEVIRMQILQAVQT 200
 |||||
 151 VKQGAENMIQMYSSGSKDRKLHGTAQQLLQDSKTKIEVIRMQILQAVQT 200
 201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAGAKNMKLLGSGKVTD 250
 |||||
 201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAGAKNMKLLGSGKVTD 250

FIG. 74

251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIEELSVA 300
 |||||G|||||KYSLEQRLNEVPKNHPKSRIIEELSVA 300
 251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIEELSVA 300
 301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRMLGCCQDILENVPGRSK 350
 |||||PRQSMISTQNQYSTLSKPAALTGTLEVRMLGCCQDILENVPGRSK 350
 301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRMLGCCQDILENVPGRSK 350
 351 ATSVLPWGPSPETRSSFMSRTSKSGSRNLLKTDDLSDNVCAVLKLD 400
 |||||WGPSPETRSSFMSRTSKSGSRNLLKTDDLSDNVCAVLKLD 400
 351 ATSVLPWGPSPETRSSFMSRTSKSGSRNLLKTDDLSDNVCAVLKLD 400
 401 NTVVGQTSWKPI SNQSDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
 |||||WKPI SNQSDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
 401 NTVVGQTSWKPI SNQSDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450

FIG. 74 (CONT.)¹

FIG. 74 (CONT.²)

```

1 MVSSQKLEKPIEMGSSEPLIADGDRRRKKRRRGRATDSLPGKFEDMYKL 50
  |||||
1 MVSSQKLEKPIEMGSSEPLIADGDRRRKKRRRGRATDSLPGKFEDMYKL 50
  |||||

51 TSELLGEGAYAKVQGVSLQNGKEYAVKIIEKQAGHSRSRVFREVETLYQ 100
  |||||
51 TSELLGEGAYAKVQGVSLQNGKEYAVKIIEKQAGHSRSRVFREVETLYQ 100
  |||||

101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGT 131
  |||||
101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGG 131
  |||||

```

FIG. 75


```

1  MSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDL  50
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
194 LGSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDL  243

   . . . . .
51  WSLGVVLYIMLSGYPPFVGHCADCGWDRGEVCRVCQNKLFESI QEGKYE  100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
244 WSLGVVLYIMLSGYPPFVGHCADCGWDRGEVCRVCQNKLFESI QEGKYE  293

   . . . . .
101 FPKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVGQAPEKGLP  150
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
294 FPKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVGQAPEKGLP  343

   . . . . .
151 TPQVLQRNSSTMDTLTFAAEAIALNRQLSQHEENELAEPEPALADGLCSM  200
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
344 TPQVLQRNSSTMDTLTFAAEAIALNRQLSQHEENELAEPEPALADGLCSM  393

   . . . . .
201 KLSPPCKSRLARRRALAQAGGEDRSPTAL  231
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
394 KLSPPCKSRLARRRALAQAGGEDRSPTAL  424

```

FIG. 77

```

1 MRKGVLKDPEIADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTSEV 50
  |||||
1 MRKGVLKDPEIADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTSEV 50
  |||||
51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
  |||||
51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
  |||||
101 MEYCLGSASDLLLEVHKKPLQVEIAATHGALHGLAYLHSHALIHR 146
  |||||
101 MEYCLGSASDLLLEVHKKPLQVEIAATHGALHGLAYLHSHALIHR 146
  |||||

```

FIG. 78


```

27 KDLVEEEAEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGP 76
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
435 KDLVEEEAEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGP 484
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

77 CHLSAWAWASWPAAACTAGPKGRPPMTQVYERLEKLQAVVAGVPGHLEA 126
   | : : : : : | | | | | | | | | | | | | | | | | | | | | |
485 CPPELGLGLQLACCCLHRRKRPPMTQVYERLEKLQAVVAGVPGHLEA 534
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

127 ASCI.PFPQENSYSVSTGRAHSGAAPWQPLAAPSGASAQAAEQLRGPNQ 175
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
535 ASCIPSPQENSYSVSTGRAHSGAAPWQPLAAPSGASAQAAEQLRGPNQ 584
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

176 PVESDESLGLSAAALRSWHLTPSCFLDPAPLREAGCPQGDTAGESSWGSG 225
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
585 PVESDESLGLSAAALRSWHLTPSCFLDPAPLREAGCPQGDTAGESSWGSG 634
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

226 PGSRPTAVEGLALGSSASSSSSEPPQIIINPARQKMVQKLALYEDGALDSL 275
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
635 PGSRPTAVEGLALGSSASSSSSEPPQIIINPARQKMVQKLALYEDGALDSL 684
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

276 QLLSSSSLPGLGLEQDRQGPKKVMNFRA 303
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
685 QLLSSSSLPGLGLEQDRQGPPEESDEFQS 712

```

FIG. 80

```

20  QTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERL  69
   |||
303 QTQACPPLSWPQRLDILLGTARAIQFLHQDSPSLIHGDIKSSNVLLDERL  352
   |||

70  TPKLGDGFLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLA  119
   |||
353 TPKLGDGFLARFSRFAGSSPSQSSMVARTQTVRGTLAYLPEEYIKTGRLA  402
   |||

120 VDTDTSFGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEAGVALRST  169
   |||
403 VDTDTSFGVVVLETLAQRAVKTHGARTKYLKDLVEEEAEAGVALRST  452
   |||

170 QSTLQAGLAADAWAAPIAMQIYKKHLDPGPGCHLSWAWAWASWPAAACT  219
   |||
453 QSTLQAGLAADAWAAPIAMQIYKKHLDPGPGCPPELGLGLQACCLH  502
   |||

220 AGPKGRPPMTQVYERLEKLAQVAVGVPGHLEAASCI.PFPQENSIVSSTG  268
   |
503 RRAKRRPPMTQVYERLEKLAQVAVGVPGHLEAASCI.PFPQENSIVSSTG  552

```

FIG. 81

```

269 RAHSGAAPWQPLAAPSGASQAQAEQLQRGNQPVESDESLGGLSAAALRSW 318
|||||
553 RAHSGAAPWQPLAAPSGASQAQAEQLQRGNQPVESDESLGGLSAAALRSW 602
|||||
319 HLTSPCLDPAPLREAGCPQGDTAGESSWGSGPGSRPTAVEGLALGSSAS 368
|||||
603 HLTSPCLDPAPLREAGCPQGDTAGESSWGSGPGSRPTAVEGLALGSSAS 652
|||||
369 SSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSSSSLPGLGLEQDRQ 418
|||||
653 SSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSSSSLPGLGLEQDRQ 702
|||||
419 GPKKVMNFRA 428
||:::|:::
703 GPEESDEFQS 712

```

FIG. 81 (CONT.¹)

```

1  MAGGPGGEPAAPGAQHFLYEVPWVMCRFYKMDALEPADWCQFAALIV 50
  |||||||
1  MAGGPGGEPAAPGAQHFLYEVPWVMCRFYKMDALEPADWCQFAALIV 50
  |||||||
51 RDQTELRLCERSGQRTASVLWPWINRNARVADIVHILTHLQLLRARDIIT 100
  |||||||
51 RDQTELRLCERSGQRTASVLWPWINRNARVADIVHILTHLQLLRARDIIT 100
  |||||||
101 AWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSSASTFLSPAFFGS 150
  |||||||
101 AWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSSASTFLSPAFFGS 150
  |||||||
151 QTHSGPELGLVPSASLWPPPPSPAPSSTKPGPESSVSLIQGARPSPFCW 200
  |||||||
151 QTHSGPELGLVPSASLWPPPPSPAPSSTKPGPESSVSLIQGARPSPFCW 200
  |||||||

```

FIG. 82

201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMNTVYAVKRLKENADLEWT 250
 ||||| 201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMNTVYAVKRLKENADLEWT 250
 ||||| 201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMNTVYAVKRLKENADLEWT 250
 ||||| 251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
 ||||| 251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
 ||||| 301 HCQTQACPPLSWPQRLDILLGTARASQVSCNRVSSCVSKSSPGL 344
 ||||| : : : : :
 301 HCQTQACPPLSWPQRLDILLGTARAIQF.....LHQDSPSL 336

FIG. 82 (CONT.¹)

1 MFTEDVKFYLAELALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFG 50
 |||||
 164 MFTEDVKFYLAELALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFG 213
 |||||
 51 LSKESIDHEKKAYSFCGTVEYMAPEVNNRRGHTQSADWWSFGVLMFEMLT 100
 |||||
 214 LSKESIDHEKKAYSFCGTVEYMAPEVNNRRGHTQSADWWSFGVLMFEMLT 263
 |||||
 101 GTLPFQGGKDRKETMTMILKAKLGMPQFLSPEAQSLRLMKRNPANRLGA 150
 |||||
 264 GTLPFQGGKDRKETMTMILKAKLGMPQFLSPEAQSLRLMKRNPANRLGA 313
 |||||
 151 GPDGVEEIKRHSFESTIDWNKLYRREIHPFPKATGRPEDTFYFDPEFTA 200
 |||||
 314 GPDGVEEIKRHSFESTIDWNKLYRREIHPFPKATGRPEDTFYFDPEFTA 363
 |||||
 201 KTPKDSPGIPPSANAHQLFRGFSFVAITSDDESQAMQTVGVHSIVQQLHR 250
 |||||
 364 KTPKDSPGIPPSANAHQLFRGFSFVAITSDDESQAMQTVGVHSIVQQLHR 413
 |||||
 251 NSIQFTDGYEVKEDIGVGSYSVCVKRCIHKATNMEFAVKV 289
 |||||
 414 NSIQFTDGYEVKEDIGVGSYSVCVKRCIHKATNMEFAVKI 452
 |||||

FIG. 83

```

1  MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEEINPQTEEVSIKEI 50
  |||
1  MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEEINPQTEEVSIKEI 50
  |||
51  AITHHVKEGHEKADPSQFELLKVLGQSGFGKVFVLVKKISGSDARQLYAMK 100
  |||
51  AITHHVKEGHEKADPSQFELLKVLGQSGFGKVFVLVKKISGSDARQLYAMK 100
  |||
101 VLKATLKVDRVRVTKMERDILVEVNHFFIVKLHYAFQTEGKLYLILDFL 150
  |||
101 VLKATLKVDRVRVTKMERDILVEVNHFFIVKLHYAFQTEGKLYLILDFL 150
  |||
151 RGGDLFTRLKSKEVMFTEEDVKFYLAELALALDHLHSLGIIYRDLKPE 197
  |||
151 RGGDLFTRLKSKEVMFTEEDVKFYLAELALALDHLHSLGIIYRDLKPE 197
  |||

```

FIG. 84

FIG. 85

```

251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
|||||
251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
|||||
301 QRVDNIEVLTADIVINLLSYRDIQDYDSIVKLVETLEKLPFDLASHHH 350
|||||
301 QRVDNIEVLTADIVINLLSYRDIQDYDSIVKLVETLEKLPFDLASHHH 350
|||||
351 VKFHYAFALNRRNLPGDRAKALDIMPVQSEGQVADMYCLVGRIYKDM 400
|||||
351 VKFHYAFALNRRNLPGDRAKALDIMPVQSEGQVADMYCLVGRIYKDM 400
|||||
401 FLDSNFTDTESRDHGASWFKKAFESEPTLQSGINYAVLLAAGHQFESSF 450
|||||
401 FLDSNFTDTESRDHGASWFKKAFESEPTLQSGINYAVLLAAGHQFESSF 450
|||||
451 ELRKVG 456
|||||
451 ELRKVG 456

```

FIG. 85 (CONT.¹)

1 MREFVLKLNHNKIVKLF AIEEETTRHKVLIMEFCPGSLYTVLEEPS 50
 |||
 53 MREFVLKLNHNKIVKLF AIEEETTRHKVLIMEFCPGSLYTVLEEPS 102
 |||
 51 NAYGLPESEFLIVLRDVGGMNHIRENGIVHRDIKPGNIMRAL 93
 |||
 103 NAYGLPESEFLIVLRDVGGMNHIRENGIVHRDIKPGNIMRVI 145

68 IGS.....AAYDAVLDNRVAIKKLSRPFQNTAKRAYRELVMKCVN 110
 ||| |||
 70 IGGAQGI VCAAYDAVLDNRVAIKKLSRPFQNTAKRAYRELVMKCVN 119
 ||| |||
 111 HKNIISLNLNVFTPQKTLEEFQDVYLVMEELMDANLCQVIQMELDHMSYL 160
 ||| |||
 120 HKNIISLNLNVFTPQKTLEEFQDVYLVMEELMDANLCQVIQMELDHMSYL 169
 ||| |||
 161 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDFGLARTAGTSFM 210
 ||| |||
 170 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDFGLARTAGTSFM 219
 ||| |||
 211 MTPYVVTRY YRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYI 260
 ||| |||
 220 MTPYVVTRY YRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYI 269
 ||| |||
 261 DOWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFP 310
 ||| |||
 270 DOWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFP 319
 ||| |||

FIG. 87

```

311 ADSEHNKLSAQARDLLSKMLVIDPAKRISVDDALQHPYINWWDPAEVE 360  

| | | | | | | | | | | | | | | | | | | | | | |  

320 ADSEHNKLSAQARDLLSKMLVIDPAKRISVDDALQHPYINWWDPAEVE 369  

| | | | | | | | | | | | | | | | | | | | | | |  

361 APPQIYDKQLDEREHTEEWKELIYEYMNSEKTNGVVKGQPSPSAQ 410  

| | | | | | | | | | | | | | | | | | | | | | |  

370 APPQIYDKQLDEREHTEEWKELIYEYMNSEKTNGVVKGQPSPSAQ 419  

| | | | | | | | | | | | | | | | | | | | | | |  

411 VQQ 413  

| | |  

420 VQQ 422
```

FIG. 87 (CONT.¹)

FIG. 88

FIG. 89

```

251 HSLPSDETFQNMNSKRKAETWKRNRQLAFSTVGTDPYIAPEVFMQTGYN 300
|||||
251 HSLPSDETFQNMNSKRKAETWKRNRQLAFSTVGTDPYIAPEVFMQTGYN 300
|||||
301 KLCDWWSLGVIMYEMMLIG 318
|||||
301 KLCDWWSLGVIMYEMMLIG 318

```

FIG. 89 (CONT.¹)

```

11 VSGGMLDIKIYIVNRGEHKNGLVEEAI IATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGMLDIKIYIVNRGEHKNGLVEEAI IATILKEVLEGLDYLHRNGQIH 192
:|||||
61 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVRKTFVGTPCWMA 110
|||||
193 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVRKTFVGTPCWMA 242
|||||
111 PEVMEQVRGYDFKADMWISFGITAEIATGAAPYHKYPPMKVLMMLTLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWISFGITAEIATGAAPYHKYPPMKVLMMLTLQNDP 292
|||||
161 PTLETGVEDKEMMKYKSFRLKLSLCLQKDPKSRPTAAELLKCKFFQKA 210
|||||
293 PTLETGVEDKEMMKYKSFRLKLSLCLQKDPKSRPTAAELLKCKFFQKA 342
|||||
211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEGDGWESDDDEM 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEGDGWESDDDEM 392

```

FIG. 90

261 EKSEEGKAAFSQEKSRRVKEENPEIAVSASTIPEQIQISLSVHDSQGPPNA 310
 |||||
 393 EKSEEGKAAFSQEKSRRVKEENPEIAVSASTIPEQIQISLSVHDSQGPPNA 442
 |||||
 311 NEDYREASSCAVNLVLRNRSRKEINDIRFEFTPGRDTADGVSQELFSAG 360
 |||||
 443 NEDYREASSCAVNLVLRNRSRKEINDIRFEFTPGRDTADGVSQELFSAG 492
 |||||
 361 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCGSEIPDEVKLIGFA 410
 |||||
 493 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCGSEIPDEVKLIGFA 542
 |||||
 411 QLSVS 415
 |||||
 543 QLSVS 547

FIG. 90 (CONT.¹)

```

11 VSGGMLDIKIYIVNRGEHKNVLEAEIATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGMLDIKIYIVNRGEHKNVLEAEIATILKEVLEGLDYLHRNGQIH 192
.
61 RDLKAGNILLGEDGSGVQIADFGVSAFLATGGDVTRNKVRKTFVGTFCWMA 110
|||||
193 RDLKAGNILLGEDGSGVQIADFGVSAFLATGGDVTRNKVRKTFVGTFCWMA 242
.
111 PEVMEQVRGYDFKADMWSFGITAEIATGAAPYHKYPPMKVLMMLTLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWSFGITAEIATGAAPYHKYPPMKVLMMLTLQNDP 292
.
161 PTLTGTGVEDKEMMKYKGSFRKLLSLCLQDPSKRPTAAELLKCKFFQKA 210
|||||
293 PTLTGTGVEDKEMMKYKGSFRKLLSLCLQDPSKRPTAAELLKCKFFQKA 342
.
211 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDDEM 260
|||||
343 KNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDDEM 392

```

FIG. 91

FIG. 91 (CONT.¹)